

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCCGCTGGGCTCCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGCCAAAGAACGCGACGCCCTGCCACC GGTCGCCGGGGCT
GGTGGACAAGTTAACCAAGGGGATGGTGGACACCGCAAAGAACGAGACTTGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCAGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCAAGACCTGTAATTGCGGACTTACCCCTAAATTATTCAAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTATTGTCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTGATAACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAACGC
TTGGCCGCCATGGCCAACCTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCACTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAATTGCCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGCGGAAAGAACCAAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSNG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCGLTNRDCGECEVGWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEEDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGGTTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGCGTCCGCCAGGCCGGAGGCACGCGCCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTCCCGCAGCGAGGAGGTCTGAGCAGC**A**TGGCCCGGAGGAGCGCCCTC
CCTGCCGCCGCGCTGGCTCTGGAGCATCCCTCTGCTGGACTGCAGGCGGAGGC
CGGGCCGCCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTACCAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTCTATGAATTCCCTGCTGGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAACAGTGCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGTTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTTAAAACATGTCAACAAGCTGAGTGCCCAGGCCGGGTGCGAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAAGTGTGACAAAGCAAACCTGCTCAACCACCTGCTTAATGGAGGACC
TGTTTCTACCCGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCGTCAAGGAGGTAATGCAATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAAGGGAGACCTCTGTTCAAAGCCTGCTGGCAGCCTGGCTGGTGACAT
GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCCTCACTAAAAAGGCCAGGAGCGGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTTCATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTCCCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTGTTCAGTGCTTGGGACAGATTATATTATGTCAATTGA
TCAGGTTAAAATTTCAGTGTGAGTGGCAGATATTCAAAATTACAATGCAATTATGGT
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAATCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTATTGTCAGATATTAGAT
GTTTGTACATTAAAATTGCTCTTAATTTCAGGAACTCTCAATACAATATATTGACC
TTACCAATTCCAGAGATTCACTGAGTATTAAAAAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATCTAAACACAATGAAATAGGGAAATAATGTATGAACCTTGCAT
TGGCTTGAAGCAATATAATATATTGTAACAAAACACAGCTCTACCTAATAAACATTTCAT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTTGTATTGCAGCTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSRLSLDKIMADPTVNPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDGFHGPCHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKPCPQCRNGKCIGKSCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGGCGTGGCGTCCGGCGTCGCAGAGCCAGGAGGCGGAGGCGCGGGCCAGCCTGGG
CCCCAGCCCACACTTCACCAAGGGCCCAGGAGCCACC**ATGTGGCGATGTCCACTGGGCTAC**
TGCTGTTGCTGCCGCTGGCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGCGTGCACGACTGTGCCCTGCCAACCTGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGCGTGCACCCCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTGGGAACGTACTGGGACAATGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACACAGCGCCTCTGGGCATGACCGTGG**GAGGGCATTGCTACCGCCTGGGACCA**
TCCGCCCATCTCCTCGGTATGAAACATGATGAAATTATACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACTGTGATTGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCTGGCCTTCCACAGCAGCTGTGGCATCCGATGTGTCT
CAATCCATTCTCTGGGACACATGACGCCGTGCTGTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCCGGTCTCGATGGTGCCTGGTGGTTCTCGCTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTGGGCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCGCAACTCCTGGGCC
CAGCCTGGGCGAGAGGGCCACTTCCGCATCGTGCAGCGGTCAATGAGTGCAGATCGAG
AGCTTCTGCTGGCGCTCTGGGCGCGTGGGATGGAGGACATGGGTGATCACTGAGGCTG
CGGGCACACGCCGGTCCGGCTGGGATCCAGGCTAAGGGCCGGAGAGGCCCAATG
GGCGGGTGA**CCCCAGCCTGCCGACAGAGCCGGCGCAGGCGGGGCCAGGGCGCTAAT**
CCCGCGCGGGTTCCGCTGACGCAGGCCCGCCTGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCCAGACCTCCAGTGGGACGGGCAGGGCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGGCCCCACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCCACCCAAATCCGTATTCTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTACTGTAACCTCCGACTCCTGGGTTCA
AGTGCACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACACCTGGC
TAATTTGTATTTGTAAAGAGGGGGTCTCAGTGTGCTGCCAGGCTGGTTCGAACT
CCTGGGCTCAAGCGGTCCACCTGCCCTCCAAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA
AAAAACCAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCRGRADDC
ALPYLGAIACYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCCTGTCCTTNGCCCCAGAACCTGCTGTCTTGACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGG**ATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT**
GTGACACCGACTTGTGCAACGCCAGCGGGCCCAGTGCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCGAGTGGGAGCCTGTCCCTGGTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCTGCAGATGGCCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCGDPASYRLWGAPIQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAGFSTLNPLVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGTCCGAACCTCTCCAGCGATGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCAGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATA CGGCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCCGGAGGGCGGCCAGGCTTCCCGAGCCGAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACGAGAACAGCTCGAGTTGTGGCTCCGCCCGACCCGCCGGACCAAGCGCACAC
GGCGGCCCGAGCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCTGGGCCGCTCCC
CACCCCTTCCCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCACTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTAGCGACTGAAGGCCCTGCAGACAACCGTCTGGAGGTGGCTGCCTCAAAA
TCTGCTCTCGGATCTCCCTCAGTCTGCCCGAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCAACTCCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTTCTGGACTTCAACAGAACCCATCCAGT
CATTGGATTTGCTGTTTATTTTTCTTTCCCACCAATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCC
GAAGTCTTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTCAAACCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAAATGC
TGGATTTCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAACATGTCAGAGTTCTCATTGCAGGAAAAC
AAATATTCAGACCATTTCACGGCTGCTTGCCTTGAAGCTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGGCTTCCGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTTCCGTGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATCCGACATGGCCTCCAGAA
TCTCACGAGCTGGAGCGTCTTGTGGACGGAACCTCCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAGAT
AAACACATTCCCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGGGATGCTGACTCAAGGGTTTGATAATCTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCTGGTTGTGACTGCAGTATTAAATGGGTACAGAACATGGCTCAA
ATATATCCCTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAAGTCCGG
GGATGGCGTCAGGGAATTAAATATGAATCTTGTCCCTGTCCTCCACACGACCCCCGGCTG
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACCTCAGCCTCCCACCCCTCTAT
TCCAAACCCTAGCAGAACGCTACACGCCTCCAACCTCCTACCACATCGAAACTCCCACGATT
CTGACTGGGATGGCAGAGAACAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTGGTGAATGATACTCCATTCAAGTCAGCTGGCTCTCTTCAACGTGATGGCATA
CAAACTCACATGGGTAAAATGGGCACAGTTAGTAGGGGCATGTTCAAGGAGCGCATAG
TCAGCGGTGAGAACACACTGAGCCTGGTTAACTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAACAGACACATTGTTCAAGGGC
CACCAACCATGCCCTCATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGTACGGGGCGCGGTGATATT
GTGCTGGTGGCTTGCTCAGCGTCTTGCTGGCATATGCACAAAAAGGGGGCCTACACCTC
CCAGAAGTGGAAATAACACGGGGCGGCGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCTGGAGATGACAGAAACCAAGTTTCAGATCGTCTCCTAAATAACGAT
CAACTCCTAAAGGAGATTTCAGACTGCAGCCCATTACACCCCAAATGGGGCATTAATTA
CACAGACTGCCATATCCCCAACAAACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGAAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTGCATTGAAACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKS~~WLI~~ISLGLYSQVS~~KLLACPSVCRCDRN~~FVYCNERSLTSVPLGIP
EGTVLYLHNNQINNAGFPAELHNQSVHTVLYGNQLDEFPMNL~~PKNVRVL~~HQENNIQTI
SRAALAQLLKLEELHLD~~DNS~~ISTVGVEDGAFREAI~~S~~LKLLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTS~~LERL~~I~~V~~DGNLLTNKGIAEGTFS~~H~~LTKLKEFSIVRN~~N~~LSHPPP
LPGTHLIRLYLQDNQINHIPLTA~~FSN~~RKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYI~~PSS~~LNVRGFM~~C~~QGPEQVRGM~~A~~VRELNMNLLSCPTTPGLPLFTP
APSTASPTTQP~~P~~TLSIPNPSRSY~~T~~PPPTSKLPTIPDWDGRERVT~~P~~PISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATT~~H~~ASYLNNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFV~~L~~VVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKD~~N~~SILEMTETSFQIVSLNNDQLLK
DFRLQPIYTPNGGINYTDCHIPNNMRYCNS~~S~~VPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGCCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCCGCTCCCACGAGCG
ATCCCCGAGGAGAGCGCGGCCCTCGCGAGGGCGAAGAGGCCACGAGGAAGACCCGGGTGGCTCGGCCCGCTGCC
TCGCTTCCAGGCGCCGGCGCTGCAGCCTGCCCCCTTCTGCTCGCCTTGAAGGAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCTCGGACAGATCGTCTCCCTCCCTGCCGAGGGCAGGGAGCGGTCACTGTGGAGGTCCATCT
CTAGGGGCAGACACGCTCGGACCCACCCCGAGACGGCCCTTCTGGAGAGTCTCTGTGAGAACAAGCAGGGCAGACC
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCITGCAATTCTTGACATTGGTCTGTGATGTCACCCGAGTGGCCTGCTCCAATATGGCAGCAGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGGCACTGTCCACCG
GCACCATGACTGGGTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGAGGGGGCCCGGCCCCCTGA
GGGAGAAATGTGCCACGGGTCTATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCGAGGTGGCTGCTA
AGGCACGGGACACGGGCATCTTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
GGAGTGGAGCCCCATGAGGACCATGTCCTCTGTGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGACGGCCACATGTGAGCACCCCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCGT
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGTAATGTGCCGGGCTCTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGGACTACTGTGCCCTCAGAAAACACGGATGTAAC
ATGAGTGTGAAATGCTGATGCCCTACCTTGCCAGTGCAGGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGCACAAGGATCAACTACTGTGACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCAGTGACCAACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTAACACGGAGGATTCCCTCGTCTGCCAGTGCTCAGAAGGCTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGATTACTGCCCTGCTGAGTGCACATGGTTGTAATACTCCT
GTGTCACATGGACAGATCTTGCCCTGCACTGTGCTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTC
GAAAATTGGACTCTGTGCTCTGGGGACACGGTTGTGAACATTCTGTTGTAAGCAGTGAAAGATTGTTGTGT
GCCAGTGTGTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAACAGGAAGATGTCCTGCCAGTATAG
ACCATGGCTGTGAACACATTGTGTAACAGTGACGACTCATACACGTGCGAGTGCTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCAGAGGAAGGATGTCCTGCAAAATCAACCCACCATGGCTGCAACACATTGTGTTA
ATAATGGGAAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACCGAAGCAGGTGCAAGAAAT
GCACTGAAGGCCAATTGACCTGGTCTTGTGATCGATGGATCCAAGAGTCTGGAGAAGAGAATTGAGGTG
TGAAGCAGTTGTCACTGGAATTATAGATTCTTGACAATTCCCCAAAGCCGCTCGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTCACTCTGAGAAACTTCACACTGCCAAAGACATGAAAAAGCCGTGCC
ACATGAAATACATGGAAAGGGCTCTATGACTGGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCGACGGACGGCTCAGGATG
ACGTCTCCGAGTGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGTAGGAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAAGCATCTTCTATGCCGAAGACATTGAGCACAATGG
ATGAGATAAGTGGAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACGTGCAAAACGGTCAACAGCCAACAGAACATCTGAGCCAGTCACCATATAATCCAAGACCTACTTT
CCTGTTCTAATTTCAGTGCAACACAGATATCTGTTGAGAAGACAACTTTACGGTCTACACAAAGCTT
CCCATCAACAAAACCTTCAGGAAGGCCCTTGGAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACAGAAGTAAGAAAATTACACAGCGTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATCGCCTGAGATACAGATGAAAGATTAGAAGATTGCGACACATTGTTAGTCATTGTTACGGATTACAAT
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTAAGTAAACAAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACACTAATGTTGAGAAGTAAACGTTGCAAGTCTTACTT
TCAGAATTCTAAGATGAATTACACAGGTGAGAATGAATAAGCTATGCAAGGTATTGTTGAAATATACTGTGGACAC
AACTGCTTCTGCCCTCATCTGCCCTTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCAAGTCTTACTT
CTGAGAACACTGGCCATAGGAAATGCTGTTTTGACTGGACTTTACCTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGACTTGTGAAACAAGTGGATTTTACAAATATTAAAATTCAACACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEAAKARD
TGILIFAIQGVQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC
EHECVNMEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGTKCAKLDSCALGDHGCE
HSCVSSEDSFVCQCFCFGYILREDGKTCRRKDVCQAIIDHGCEHICVNSDDSYTCECLEGFR
LAEDGKRCRCKDVCKSTHHGCEHICVNNNGNSYICKCSEGTVLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQLLSCSNFAVQHRYLFEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGGGCTGGCGCCCTGACTCCGTCCGGCAGGGAGGGC
CATGATTTCCCTCCGGGGCCCTGGTACCAACTTGCTGGGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCTCGCGGGCCCAGCTGCAACTGCACCTGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTCTCAGCGTGGTACACCTGCACGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTCGGGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTCAAGACAAACAAGCAAATCTAGGGCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCAGGCCAC
AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC
AGTGGTTGCTGGAGCTTTGTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCCTGCCCTGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC
TTCCTCTGTCACCTCCGCACGAGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCC
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTTATGATGAC
CCCACCACTCATGGCTAAAGGATTGGGCTCTCCCTATAAGGGTACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTATGAAGGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCAGTCTCCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGT
ATTGATATAACCTGTGAGGCTGGCTGGTTAGGTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAAAACTAACATGAAATATGTGTTTTCTTGCAAATTAAATAAGATAACATAA
TGTTTGATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACNCVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPPIPGGVSSSGLSR
MGAVPVMPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCTAGTGTTTCCACTTG
TTGAATTGTCCTATACTCAAATTGCACCAAGACACCTTGTCTCCCAAATGAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTTGAAATTAACTCAGTCTGTGGCGAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTGCCATT
TAGATAATGTCGTATAGCTGCAAATATTAAATAAAACTTAAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAAATTGAAAACCCTGAAAT
AATTTGTTCAAAGGGATACATTGTAGTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCACACTGTTGAACAAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTTGAT
TCATATAACATGAAACATATTCTATGAAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTTATATTATA
AGAGTATTGGTCTTGTCTTCACTCTGACAACCTTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTCAGTAAATTCTCAGTCTCAATGAGCTAAACCC
ACCCACATTATATGAACTGAAAAAAATAACATTACATTAAACTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCAATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGTCCTTCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTCTTGCCATATGCATTTT
ACCTTCTGGTTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAATCTTGCTG
TAGCCTATTCTGCTGAATTGTTCTTGTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATGCCGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTATCTATTGTTGGGTGTCATCTACAAACAAGGGATTTGCA
CAAGAATTATATCTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTGGCAGCAC
TAGGATACAGATATTGGCACAAACCAAGTATGTTGGCTTAGCACCGAAAACAACCTTATT
TGGAGTTTATAGGACCAGCATGCCAATCATTCTGTTAATCTCTGGCTTTGGAGTCAT
CATATACAAAGTTTCTGTCACACTGCAGGGTTGAAACCAGAAAGTTAGTTGCTTGAGAAC
TAAGGTCTTGTGCAAGAGGGAGCCCTCGCTTCTGTTCTCGGCACCACCTGGATCTT
GGGTTCTCCATGTTGTGCACGCATCAGGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTTCCAGGGATGTTCAATTGTTATTGTCCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGTCCTGTTGGATGTTAAGGTAAACATAGAGAATG
GTGGATAATTACAACGTGACAAAATAAAATTCAAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCAAATTATAACTACTAGACAAAAGTATTAAATCAGTTCT
GTTTATGCTATAGGAACGTAGATAATAAGGTAATTATGATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGAGATATTGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCACCAAGGAAAGATTTCTTCAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC
CCTACCACCTCGTAATGAGCTCATTACAGAAAGTGGAACATAAGAGAACAGGGCAGA
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAAATGAACTGTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAAACACATTACCAATTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTTCTGTTGCTAAATCTGTTCT
TTCTAAATATTCTAAAAAAAAAGGTTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSNQDRFITNDGTVCIENVANCHLDNVCAA
NINKTLTKIRSIKEPVALLQEYVRSVTDLSPTDIITYIEILAESSSSLGYKNNTISAKDTL
SNSTLTEFVKTVNPFVQRDTFVVWDKLSVNRRTHTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAFAFLYYKSIGPLLS
SSDNFLLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCIIAGL
LHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSaalgyryygt
TKVCWLSTENNFIFSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTCCAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTGCATTTCATTATAAGAGTAT
TGGTCCTTGTTCATCATCTGACAACCTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACATTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCCTGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTCACCTTC
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGC CGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGTCA CCCGGCTGGGA
CAAGAACGCCGCGCCTGCCTGCCCGGGCCGGGGAGGGGGCTGGGGCTGGGCCGGAGGC
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCCATAAGAAATGCTCGG
TGTCTGGCACCTACCGTGGGCCGTAAGCGCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCGCGTCAGAGCAGGAGCGCTGCCTCAGGATCTAGGCCACGACCATCCAAACCC
GGCACTCACAGCCCCGCAGCGCATCCGGCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCAGAGCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCTCTGGCTGGCGTGGCCGGCGCCCCCTCGCCTTCTCGGACGCCGG
CCACGTGCACTACGGCTGGGCGACCCCATTCCGCCTGCCTGCGCACCTGTACACCTCCGG
ACGGGCTCTCCAGCTGCTTCCTGCATCCGTGCCAGGGCGTGGACTGCCGCCGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCACCGTGGCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCGACGGCAAGATGCAGGGCTGCTCAGT
ACTCGGAGGAAGACTGTGCTTCAGGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGTCTCCCTGAGCAGTCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCACTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGGAAACTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAACT
GAGACCATGCCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGACG
TGCTCTACAAGAACAGTCCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTGAATACTCCATCGATGGGAAC
TCACTTCTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCATCAGTCCACTCTGTA
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTAATTTCAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCACTCAACCCATGTGGAAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGCCACCAG
GCTTCAGGAGTAGGGAAAGCCTGGAGGCCACTCCAGCCCTGGACAATTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTGCTGTCCCGGTGTCACCTGC
TTCCATCTCCAGCCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGCCT
CCCAGGCCCCCACCCTATGTCAACCTGCACCTCTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTGCTGTGGAAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTTGGTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTTCCTACATTATTATGCCCAAATTATATTATGTATGTAAGTGAGGTTG
TTTGATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEET
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAACGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAGGCCTATGGGTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGACTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAACTGGGTGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCATAATATCCG
GATCAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACTGACTCTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAGTGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCGTGAAGCCGCAATT
TGTTGGATATCGCAGGTGCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTCACGCCGTAAATCCAGCAGTTGGAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCAGACCAGTCTGCCAATATGGTGAACCCC
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGCAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAATA
AATAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGTATTC

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQ
GQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD
GIRLLENPRLGSQSTNSSYTMNTKTGTIQLQFNTVSKLDTGEYSCEARN
NSVGYRRCPGKRMQVDDLNI SGIIIAAVVVVA
LVISVCGLGV CYAQRKG YFSKETSFQKSNSSSKATTMSENVQWLTP
VIPALWKA AAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCGGACCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA
TTGACAAATGCAAGCATCTCCTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAACTCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGAAATCAGGCTTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCAGATTGCC
AGCTAACACACAGATTCTCCTACAGACTAACAAATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTTCAGTCACCAAT
ATTAATGTAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA
ACTGCCTGAAAATGTCGTCCGAACTGAGCAACTACAAGAACTCTATATTAACTACA
TGCTTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCATGT
TGCTCTCCTAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAATAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATATGCC
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACCAACCCTAGATTGTCTTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGGTACGCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTACTGTGTCATCCGGTG
GATGAACATGAACAAAACAAACATTGATTGACAGACAGAAGTTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTAGAATGTTGGCAAGTGCATTCAGGGACATGATGAAATTGT
CTCCCTCTTATAGCTCCTGAGAGCTTCCCTTAATCTAAATGAGAGCTGGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACCAACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAGAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATATAATGGCGTAACTCCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT
GGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAGAGATATTCAAGGCCATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGGCAAAGTGCAGAACATCCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAAATGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
ACAACACATTGGCCTGTCTGGAGGCCTTCTGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCCTGTATAAATCTCTGGAAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGCAACTGTATAGGTTACCAACAAATATGTCCT
AAAAACCAACCAAGGAAACCTACTCCAAATAATGAAC

FIGURE 26

MKDMLPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLLQTNNAKIEYSTDFFVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLSNRQLMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFDDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLPSTEYKICIDIPTIYQKNRKCVNVTKGHLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCC GG ACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTGTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTTAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGCATTGCAGTAGAAATAAGTGGTTACTTCTCCATTGTAAACACATTGAA
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTT
AATTAAAAGCAAATAAAGCTTAACTTGAACCATTGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSDNQITSIPNEIFKDLHQQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGC~~GCGCCGAGATG~~CAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGT~~GAGGAGCATGCC~~AGCCCCCTCCTGGC~~CTGGCAGCCC~~ATCCTCCTGCTGGTGCT
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGT~~TTGTGGCAGT~~CCCCGAGGGCATCCCCACCGAG
ACGCGCTGTGGACCTAGGCAAGAACCGCAT~~AAACGCT~~CAACCAGGACGAGTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTAACGAGAACATCGTGAGGCCGTGGAGGCCGCG
CCTTCAACAACCTCTCAACCTCCGGACGCTGGTCTCCGAGCAACC~~GCTGAAGCTCATC~~
CCGCTAGCGCTTC~~ACTGGCCTCAGCAAC~~TGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTT~~CAGGAC~~CTGTACAACCTCAAGTC~~ACTGGAG~~TTGGCG
ACAATGACCTCGTCTACATCTC~~ACCGCGC~~TT~~CAGCGGC~~CTAACAGC~~CTGGAG~~CAGCTG
ACGCTGGAGAAATGCAAC~~CTGAC~~CTCCATCCCCACCGAGGGCTG~~CCCAC~~CTGCACGGCCT
CATCGT~~CCTGAGG~~GCTCCGGCACCTCAACATCAATGCCAT~~CCGG~~ACTACTC~~CTTAAGAGG~~C
TGTACCGACTCAAGGT~~TTGGAG~~ATCTCCACTGGCCTACT~~TGGACACC~~ATGACACCCAAAC
TGCCTCTACGGC~~CTCAAC~~CTGAC~~GTCC~~GTCCATCACACACTGCAATCTGACCGCTGTGCC
CTAC~~CTGGCGTCCG~~CCAC~~CTAGT~~CTATCTCG~~CTC~~CAAC~~CTCT~~ACAAC~~CCC~~CATCA
GCACCATTGAGGGCTCCATGTTG~~CATGAG~~CTGCTCCGGCTGCAGGAGATCCAG~~CTGGTGG~~GC
GGCAGCTGGCGTGG~~GGAG~~CC~~CTATGC~~CTCCGGC~~CTCAACTAC~~CTGCG~~GTGCTCAA~~
TGTCTCTGGCAACCAG~~GTGAC~~CAACTGGAGGAATCAGT~~CTTCACTCGG~~TGGGCAAC~~CTGG~~
AGACACTCAT~~CTGGACT~~CCAAC~~CCGCTGGC~~ACTG~~TGCGACT~~TG~~CGGCT~~CTGTGGG~~TGTTCCGG~~
CGCG~~CTGGCG~~CTCAACT~~CAAC~~CCGG~~CAGCAG~~CCC~~ACGTGCGCC~~ACGCC~~GAGTTG~~TCCA
GGCAAGGAGTTCAAGGACT~~CCCTGAT~~GTG~~CTACTG~~CCC~~AACTACT~~T~~CAC~~CTGCCGCCGCG
CCCGCAT~~CCGGGACCG~~CAAGGCC~~AGCAGG~~TGTT~~GTGGAC~~GAGGGC~~ACACGG~~TGAG~~TT~~
GTGTGCC~~GGGCCG~~ATGGCGAC~~CCGGCC~~CC~~CATC~~CT~~GGCT~~CTC~~ACCCCC~~AAAGC~~ACCT~~
GGTCTCAG~~CCAAGAG~~CAATGGG~~GGCT~~AC~~AAGT~~T~~CTCC~~GT~~ATGG~~C~~AGCTGG~~AG~~GTGCG~~CT
ACGCC~~CAGGT~~AC~~AGGACAACGG~~CAC~~GTAC~~T~~GTG~~C~~ATCG~~CCGCC~~AAACG~~CGGG~~GGCAACG~~AC
TCCATGCCGCC~~CCAC~~CTG~~CATGTGCG~~C~~AGCTACTCG~~CC~~GACTGG~~CCC~~CATCAG~~CCC~~AAACAA~~
GAC~~CTCG~~CT~~TCATCT~~CA~~ACCAG~~CCGG~~GAGGGAG~~GG~~GGCAAC~~AGC~~ACGCC~~CC~~GGCCACTG~~
TGC~~CTTCCC~~CTCG~~ACATCA~~AG~~ACCT~~C~~ATCATCG~~CC~~ACCAC~~ATGG~~GCTTCATCT~~TT~~TC~~
CTGGG~~CGT~~CT~~CTCTG~~C~~CTGGT~~G~~CTG~~T~~GTGTT~~CT~~CTGGAG~~CC~~GGGCAAGGG~~CAAC~~AC~~
AAAGCACAACATCGAGATCGAGT~~ATGTG~~CCC~~GAAGT~~CG~~GACG~~C~~AGGC~~CAT~~CAGCT~~CCGCCG
ACGCG~~CCCCG~~CAAG~~TTCAAC~~ATGAAG~~ATGAT~~T~~GAGG~~CC~~GGGG~~GG~~GGGG~~CA~~GGGAC~~CCCCG
GGCG~~GGGG~~CA~~GGGG~~AA~~GGGG~~CTGGT~~CGCCAC~~CTG~~CTACTCT~~CC~~AGTC~~CT~~CC~~AC~~CTC~~
CTCC~~CTAC~~CC~~CTCTAC~~AC~~ACGTT~~CT~~CTTCT~~CC~~CCGCT~~CC~~GTC~~CC~~CTG~~CT~~GCCCCCG~~
CCAG~~CCCT~~CA~~CC~~CTG~~CCCT~~CC~~CTAC~~AG~~GACCT~~C~~AGAAG~~CC~~CAGAC~~T~~GGGGAC~~CCCCA
CCTACACAG~~GGGC~~ATTG~~ACAGA~~CT~~GGAG~~T~~GAAAG~~CC~~GACGAAC~~CG~~ACCGAC~~CG~~GCGCAGAG~~TCA
ATAATTCAATAAAAAAGTTACGA~~ACTT~~CT~~CTGTA~~ACT~~TGGTT~~CAATAATTATGG~~ATTT~~
TATGAAA~~ACTT~~GAA~~ATA~~ATAAAAAAGAGAAAAAA~~ACT~~AAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELMENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSIHCNLTAAPYLAVRHLVYLRFNLNSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSIGNQLTLEESVFHSVGNNLETLILDSNPLA
CDCRLLWVFRWRNLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACCGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCGGGAAAGCGCGATGGGGGCCCCAGCCGCTCGCTCCTGCTCCTGC
TGTTCGCCTGCTGCTGGCGCCGGCGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCCACATCACTGGTT
ATAAAATCTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGAACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGGATGATGGGGCGAGCAGTCGTGCTCTGTGAACCAGTAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCAGAAGCTGTTGCTACACTGTGAGGGTCGCCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCCTCAACAAGAGTACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCGTGGGGATCGTGGCTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTTCCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCCAAAGGCTCCGACGATGCTCCAGACGCCAGGGCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCATAGAGGCCCTGCCACTTCCTGC
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCCTCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCTTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTTGAAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGGCTTTGGATTCTGTT
GCTGGAGACGCTCTTTGCCGCTGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTACCATTTATTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTGCTAATTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTGATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAAGCCTG
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCT
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGCTGCGAAGCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAACAGAACCTTGCTCCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCTGCCCTGGGGCTGCAGCTGCCACACATCCCAGGGCTGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCCCTACGAGATAACAAGATCCACAGCATCGAAAATCGACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGCTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCACGGAAACCCCTGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT
TAGAAAGGATTTCATGCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACTCGACAGTAAAACAGCACTGGGTTGGCGAGACCGGGACGCACCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGTGTGGTCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCTTCACCGTGGTGGCATGCTCGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGAGGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GAACCTCCTACTGGCACAATGGCCTTACAACGCAGATGGGGCCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTTAAGACCCCAACCCAAATAGGGGAGGGCAGAGGGAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTGCTGAGAGCCCTTTGACAGAAAGCCCAGCAGCACGACCCCTGCTGGAAAG
AACTGACAGTGCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCCGCGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDCVCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDILNKLEVLIILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTFKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCNNRVSSLADLKP
KLSNVQELFLRDNIHSIRKSHFDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNIAIQLILPGTFNAMPKLRILILNNNLLRSLPVDFAGVSL
SKLSLHNHYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDIECPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL
VPGLLLVFVTSAAFTVVGMLVFLRNRKRSKRRDANSSASEINSLQTVCDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTCGTCCCCGTACCCGGCGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCAGGGCCTGGCAGCGCTCCGCACACATTCTGTCGCCCTAAAGGAAACTGTTGGC
CGCTGGGCCGCGGGGGATTCTTGGCAGTTGGGGGTCGCTGGAGCGAGGGCGGAGGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCCTGGGGCCTCAG
AGAATGAGGCCGGCGTTGCCCTGTGCCTCCTCTGGCAGGCCTCTGGCCCGGGCGG
CGGCGAACACCCCACGCGCACCGTGCTGGCTCGGCCCTGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCAGGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGCGCTGTGCGCCTGCGCTCCTGCGGGCAGGCCAGG
GCCCGGAGGGGCTCAAAGACCTGCTGTTCTGGGTCGACTGGAGCGCAGGCCTCCACT
GCACCCCTGGAGAACGAGCCTTGGGGGTTCTCCTGGCTGTCCTCCGACCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGAGATGCGC
GGTACTCCAGGCCACCGGTGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCCGG
GCCGCCCTTAACCTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTGGGCGATGTGTTGTCCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAC TGCC TAGACGACTTGGGAGG
GCTTTGCCCTGCGAATGTGCTACGGCTTCGAGCTGGGAAGGACGGCCGCTTGTGACCA
GTTGGGAAGGACAGCCGACCCCTGGGGGACCGGGGTGCCAACAGGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGTCGACGAGAACGCTGGAGAGAC
GACCACTTGTCCCTGAACAAGACAATTCACTGAGCTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCTCAAGCCGAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAACCTACGACTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTTGGTATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAGAAAGCCCTCTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGAATCCTGAGCCGCTGCTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGGGGACAGAG
CAGAGGGTGCCTGCTGGCGAGTCCCTTGGCTCTAGTGATGCATAGGGAAACAGGGAA
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAACTGACAATTCTGCAGAAATCCCCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGAAGTGCCTTGGAGAA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGAATTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGGAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALEERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG
ASNLSYRAPFQLHSAAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCP
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTSSATPQAFDSSSAVVFIIVVSTAVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGATT CAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATACTGCCTTAAAAGTGCCTCCGCCCTGCCGGCGCTATC
CCCCGGCTACCTGGGCCGCCCGCGCGGTGCGCGTGTAGAGGGAGCGCGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGTGGGTGCGGA
GGGGCGTGTGCGCGCGCGCGCGTGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGCTGCCACCCAGCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGAAAATCA
CAGTCCCAGAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGCCATGCCAATGCCAGCGCATTGGCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGTGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCCGCTGTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAAGTGGCCAGACCGGATTACCTGCAGGAGTCACTTGTGTGGCACATTGTAGGCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGCCGGGAAGTCACAGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTCA
TTTATCAGACTTAAGTTAACTGCAGATGGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACAGAACAGCCTGTCAACCACCATCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGAATTGTATTAGCCGGACTGTTACAAACCATACTCGCGATGGGAGTTG
CACGCCACAGTCTCGATCATCACAAAGAGGGAAATTGGCGATTCAAGCAGGCC
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCAGAAGAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACAGCTCCTGGATGCCCTAAAAAATAAGCAATG
TTAACAGTGAACGTGTCATTAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTC
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCCTGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTATTACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTAGAAGTGCACATTATAGT
GTTATTTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCGTTCTA
AATCAATGCTAATAAAATATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACCGTGGCGGACCGTGGCGGCCACGGCGCCGCGGGCTGGGCGGTGCTTCTT
CCTTCTCCGTGGCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACACTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAACATTGTCCAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTCGAGTGCCACGCCCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGTACGGCAGTGTGAAGGAGAAGG
GACACGAGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGCCCCAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCAGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCA
CGCTGGCTGCTAAGGGCAGTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCAGTGCACCGTGTGGAGGGCTCATCAAGGGCAGA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGGGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGAAGTAGC
CCTGAAGGTGGATACCATGAGCTTCACTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT
TCTGTGTTACACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLPQPIWLQPSPPPQQSPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPAGTERPCGGYQCEGEGTRGGSGHCDCQAG
YGGGEACGQCGLGYFEAERNASHLVCASFPCARCSGPEESNLQCKKGWALHHLCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKCQCENTEGGYRCICAEGYKQMEGI CVKEQI PESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLRSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTTTGCTCCCTCAGGGCA
GCACCATGCCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGAGGCCGTGCTGCCCTTCCAGG
AGCCGGTCCCCAAGGCCCGCTGCACAGGCACGGGGCTGTCCCCCGCGAGCGCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCCGTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACCGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTTCTGGGCCTCGACAGTGCATGCCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCAAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCACAGGAGGCTCCAGCCATAGGCCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGTGATGGACAAATGCTCTGTGCTCTAGTGAGGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAACTTTGCCACTGGA
GAGCCCTTGCTCAGTTCTATTCTATTCACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCCTGTCAC
TGGATCTGGCTAAAGTCCTCCACCACCTCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCATCCAGATAATAAGACTTGTAAAACATGAATAAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPHRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQSVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCCRQPPEALAFKWP
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTCACACTTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTCCCCGTGTGGAGTGGAGTTGACCA
AGGAGACACCACCAGACTCGTTGCTATAATAACAAGATCACAGCTTCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGGGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTGCCACCATTGGGAACCGGG
CAGTGCCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT
GGGATAGTGTGCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTTCTATGTCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAAGCTCTGATACTGGAGAATACA
GCTGTGAGGCACCGGAATGGGTATGGACACCCATGACTTCAAATGCTGTGCGCATGGAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTTGTAAACCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTCCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCATTGGTCTTC
TACACCCCACAGGGCCCTACTCTTCGATGTGTTAAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGAAAAATGGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTTGGTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTTCTGTCTTCCATGGGAAGTG
CCACTGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG
GATTAAAACCGCTGCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCC
TAATCCCAGAGGCTGAGGCAGGCCGATCACCTGAGGTGGAGTCGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLCYNNKITASYEDRVTFPLPTGIFTKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEEKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCCGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTCCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTATGCGTGCCCCCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACGCCCTGGCCTCCCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGCTGCACGGCCA
CCCAGACTGTCCCAGTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGGCCAACTGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTCACGCCACCCCTCCTCCTTGTCCCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCTGAGGACAAGCAACTGCCACCCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCCGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGCCCTGGAGATTGAGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRLLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTLRNATTMGPPVTLESVPVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACCGCGTCCGGTCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAAGTGA
TAATTCCATCTGTGTGCAAGAACGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA
ACAAGACATATAGACATGGAGAGAACGTAATCATCACTTGTCAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTATGTGCGCATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTGAGTGCTTACAAAACCTTATCTGGTGTCCAGGCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCGTCT
GCCACCCGGCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTACTGCGATCCT
GGCTACAGCCTCACCACCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCCCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCTTAGGCCCGGGTACATGGCCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGGACAACCTGACATA
ATTGCCAGCAGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGGTTTAGACAAATGTAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDFLEQQQQQQQPQSPQRILLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD'TDGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASNDPIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGC~~CC~~CTCCCCCGC~~CC~~TGGTCCGTGGTGGCTAGAGA
TGCTGCTGCCGCCGGTTGCAGTTGTCGCACGCCCTGCCGCCAGCCGCTCCACGCCGT
AGGCCCGAGTGTGGGGGCCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGGTGGGCCGACGGGTCGCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTAA
TAAAGTCATTACTTCATGATACTTCTCGAAGACTGAACTTGAGGAAGCAAAGAACCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTTGCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA
GGAGAAAACAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATA
CACAATTAGGAAC~~TGGTATG~~GGATGAGCCGTCTGCCAGCAGGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCAATTGCAAATATTCTGATGAGAAACCAGCAGTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCTCTCCTCCTTGTGGTACCAAGTGTATGTTGGTT
GGATCTGTAGAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTCAATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTGGTTGTATCTAACTTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTCTGCTATACAG
CAGCACATATTATCATAACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGFHWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEAKKTFKESREAALNAYILIPSIPLLL
VTTVVCVWWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFS
PDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTTCAAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGCGGGTGGCCCTGGCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTAGAAGTCTTGATCCAACTACCAAAGCTGGAGCCTGA
GGCAGAGAACAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT
GGACAACGTGGCTGCCAGGCAGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGGAACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCAACAGATCAGAAAGCTGTATCTATGCCGCTCATGATG
TGACCTTCATACCGCTTTAATGACCTGGGATTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCAACGGGAAGGAGCAGGTGCCAGAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLIES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LDMLNAMS VYTLSPEKYHALCSQTQVM EVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTGCAGCTAAACTAAATATTGCTGCTGGGACCTCCTTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGGGGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAAGGCCAGTGGGGCACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGCCGAAAACCCATCTGGCTGAGCCAGATGTCACTGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTGGGGAAAGAACACCTGCAACCAGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACACCTCTGCTCTGGCGACTG
GAGGTGCTGACAAGGGCTATGGGCTCTGTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCAGCACAGATTGGGGTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACACTACATCA
CCACCTTCATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGAACCTTATTACAATAATAAGATAGCAC
TATGTGTTCAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCCRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

0 9 9 0 0 0 6 4 1 6 3 2 4 1 6 3 2 4

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGCGTCCCGGGACCGTGGCGGACCGTGGCCGGTACCAAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGGGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGG
TGTGGACAAGAGGGTATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCCACAGGCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACGAGCACTCTTAGGTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTAATGGAGATTGTCTACAAGTG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA
AGCTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGATGGCCAATTGTTATTGCAGCTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKEAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTVDKRMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVN
AITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAAACGCTCGCAGCCACAAAAGGGATGAATTCTTCTGGACATCCTC
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCAGAACATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GACTGACTGCCATGAAATTGCTAAACTTAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGAACAGCTGCCAATGCAAGGACTGGTGCCAAGGTTACACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTAATTGCACTGACATTCTGGACTACAAA
GGCATTTCTCTGCAATGACGAAGAATAACCATGCCATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCGGTCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATAACTGGAGTCAAAACAATG
TCTGTCCTAATTGCAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTT
CCTGGAGTTAAAAGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTCTGAAAAGTGAATTACCAAGGTTAGGTTGATGTCATCTA
ATAGTGCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTCAATA
TCATTGAGGCTTGGCAGTCTCATTACTACCACCTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGGCTCACCTGAAGGCTTGCAA
AATTGTAACCATACCGTTATTAAACATATATTATTATTGATTGACTAAATTGTTG
ATAATTGTTCTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTAAATAAA
TGAAGGACTATATCTAGGGTATTCAACATGAATATCATGAACCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATAACCTCACATTCCAATGCCAAACATTCT
GCACAGGGAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAAAATGGATCACACTTAAAAAAA
AA
AA

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACCGCGTCCGGACCGTGGTCGACTAGTTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTCGCGCCGACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCTGGCCCCGTGATGGGCTGTTCGCTCCCTATA
CAGAAGTGGGAAGATCCAAAAGGAAGAGAAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTAACACAGCAACCTCTTCTGGTC
TTCCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCTTATGTTGTACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTGCACTATTAGTTCAGATATTCCCTGAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACCGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAACAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGCTAAC
AAAGTGTACCTTCTTACCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGGGT
GCACCGAACCTGAGGATCAGCTTACTATGTGAAATTGGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACATAGTTGAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAGCCATGGTTAAGTGAATAATTATAAGGTCTGA
TCTACAATGCCAAGTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAAATTATC
GAGGTGGAGGACATATTACCTATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCATTATGAAAAGGATGGATGGCTTATGTTGATAAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTTGAAACAAGTGAGC
TTTGTTTGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTAGGGCTTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYEAGKIQKGREL
VGPFPGNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTLSMLYIDNPVGTGSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNPNVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAAALTERSLMGMDWKGSQEYKKAEKVVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGGCTACAAACAT
TTTCCCTTCCTAACAGTTAACAGCTGTTAACAGCTAGTGATCAGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGACTCTCACTCAGGGTGACCAGCTCCTT
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCAGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCCTGCTAACAAAGCTTCAAAAACAGGAGCGACTTCCACTGGCTGGGAT
AAGACGTGCCGTAGGATAGGGAAAGACTGGTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTCTGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTAAAATTTAAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA
GAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCCCTGGTC
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTGGTCTGACCACTCTGCCTTGTGTTT
GCAGAAATCATGTGAGGGCAACCGGGAAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGGTCTGCTCAGTGGCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC
ATGCCTCAGTCAGCACCTCCACTCTGAGAATCGTACTGGACCTCAACCAACTTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCAGGCTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCAGAAGAGGACAACAAGTCTGTTACCCG
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGCACCCCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTTACCAAGGGGTCTGCA
AGCTGCTGCGCTGGATGACCTCTCATCCTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCCA
GCCGGAAGCTGCCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTTGACAT
CTTCACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCAGCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATGTGCGG
CTCTGCAAGGATGACCCCAAGTTCACTCATACGTGTCCCTGCCCTGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGCTACCTGGCAAGCCTGGGACTCACTGGCC
AGGCCTTCAATATCACCAGCCAGGACGATGACTCTGCCCTGTGCTGCCCTATCCGGCCATCAACTT
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGAAAAGGTAAGAGTCTATGAGTCAGATGCTCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTATTTCTTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGGTTAATTGTG
ACTTAGCTTCTAGCTACTTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAGAAAAACTTAAGGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWLLAPPAAGMPQFSTFHSENRDWTFNHLTvhQGTGAVVGAINRV
YKLIGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLNNVNKLIIIDYSENRLLAGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPARDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHsYVSLPGCTRAGVEYRLLQAAYLAKP
GDSLAAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEQN
LELNWLLGKDVKQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGC GG ACTGGAGTGGGAACCCGGTCCCCCGCCTAGAGAACACCGCATGACCA
CGTGGAGCCTCCGGCGAGGCCCGCACGGCTGGACTCCTGCTGGCTCTGGCTTCTGGCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGGGCTCCGCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGCTCCATCCACTATTCCTGTGCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTTGAACACCCCTCACCACTATGTTCCGTGAAACCTGCATG
AGCCAGAAAAGAGGCAAATTGACTTCTGGAACTGGACCTGGAGGCCTTCGTCTGATGGCCGCAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTAACAGGGCTCACCGAAGCAGTGGACCTTATTGACCACC
TGATGTCAGGGTGGTGCACCTCAGTACAAGCGTGGGGACCTATCATGGCGTGCAGGTGGAGAATGAATATG
GTTCCATAATAAGACCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCTGGCATTGTGGAACACTGC
TCCTGACTTCAGACACAAGGATGGCTGAGCAAGGGGATTGTCAGGGAGTCTGGCCACCATCAACTTGCAGT
CAACACACGAGCTGCAGCTACTGACCACCTTCTTCACGTCAGGGACTCACGGGCAAGATGGTGTGAGT
ACTGGACGGGTGGTTGACTCGTGGGAGGCCCTACAATATCTGGATTCTCTGAGGTTTGAACACCGTGT
CTGCCATTGTGGACGCCGGCTCCCATCAACCTCTACATGTCACGGAGGCCAACATTGGCTTCATGAATG
GAGCCATGCACTTCATGACTACAAGTCAAGTGTACCCAGCTGATGATGTCAGGGAGTCTGGCCACCATG
ATTACACGGCCAAGTACATGAAGCTCGAGACTCTCGGCTCATCTCAGGCATCCCTCTCCCCCACCTG
ACCTTCCTCCCAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGTCTCTGTGGGACGCCCTCAAGTAC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT
TCGGGTACATTCTATGAGACCAGCATCACCTGCTGGCATCCTCTCAGTGGCCACGGTGCATGATGGGGCAGG
TGTGTTGAAACACAGTATCCATGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCTGGGATG
ACACCGTGTGAGGATCTGGTGGAGATCGTGGGGGACTCAACTATGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGAAATCTCTATCGAATGATTCAACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCATTGAGGTTGGCTGGACAAATGGNGTTCCCTCCAGAAACACCCACATTACCTGTTCTCTGG
GTAGCTTGTCCATCAGCTCCAGCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGGTTGTATTCA
TCAATGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTATCGTTTGAGGAGACGATGGCGGGCCCTGCATTACAGTTCA CGGAAACCCCC
ACCTGGCAGGAACCAGTACATTAAGTGAAGCGGTGGCACCCCTCTGCTGGTGCAGTGGGAGACTGCCCTC
CTCTTGACCTGAAGCCTGGCTGCTGCCACCCCTACTGCAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCTTAAGCCTGCAGGGAAAGGTGGATGGCTCTGGG
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTCTGTGCCAGGGCTGTGGCTCTAGGGTGGAG
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGTGAAACCTGGCCCTTGCAAGGGACGTACAGGCC
TGGCAGGACATCTGCTGGACTCAGCGTGTCTTGCTGGTCTGGGAGGCTGGCCACATCTCTCATGGCCCC
TTTATCCCCGAAATCTGGGTGTGTCACAGTGTAGAGGGTGGGAGGGGTGTCTCACCTGAGCTGACTTGT
CTTCTCTACAAACCTCTGAGCCTCTTGGGATTCTGGAAGGAACTGGCGTGAGAAACATGTGACTTCCCCT
TCCCTTCCACTCGCTGCTTCCACAGGGTGACAGGCTGGAGAACAGAAATCCTCACCCCTGCCTTCTCC
CAAGTTAGCAGGTGCTCTGGTGTGAGTGGAGGACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGC
CATCCAGGGAGGGAGGACAGAAGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCACATCC
AGGGAGGGAGGACAGAAGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGG
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGGCCAGAACAGCAGGGGAGGAGCAGGCCCTCTTC
GAAGTGTGTCAGTCCGATTGAGCCTTGTCTGGGGCCAGGCCAACACCTGGCTTGGGACTGTCTG
GTTGCAGTAAAGCTATAACCTGAATCACAA

FIGURE 64

MTTWSLRRR PART LGLLL VVLGFLV LRR LDWSTLVPLRLRHRQLGLQAKGWNFM LEDSTFW
I FGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWLH EPERGKFDFSGNL DLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFT EAVDLYFDHLM SRV VPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTS DNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVMEYWTGWFD SWGGPHNILD SSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTA KYMKL RDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNQSF GYI LY
TSITSSGILSGHVHD RGQVFVN T VSIGFLDYKTTKIAVPLI QGYTVL RILVENRG RVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXSLP EPTLPAFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLS SGINQVIVFEETMAGPA
LOFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315, 320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGTGACGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCGCCGTCTCAGACTAGAGGAGCGCTGTAACGCCATGGCTCCC
AAGAACGCTGTCCTGCCTCGTCCCTGCTGCCGTAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGTCGTTGCTAGTGGATAGGGTCATGACCGTTCTCCTAGACGGGCC
CGTCCGCTATGTCCTGGCAGCCTGCACTACTTCGGTACCGCGGGTGCTTGGGCCAC
CGGCTTTGAAGATGCCATGGAGCGGCCAAGCCATACAGTTATGTCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGGCCACCTCATTGCCCTTCTGA
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCATCTGGTGTGTTGAAAACCTGAAATTCTAAGAACCTC
AGATCCAGACTTCCTGCCAGTGGACTCCTGGTCAAGGTCTGCTGCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTTCCGTGACTGCTAGG
AGAAAAGATCTTGTCTTCAACCACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCGGG
GAECTATACCACTGTAGATTTGGCCAGCTGACAACATGACCAAAATCTTACCTGCTT
CGGAAGTATGAACCCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCCTCGATTACTACAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCACACCTAACGTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTGGCATTACTGGCTTCCTAGACTGCTTGCCCCGTGGGCCAT
TCATTCAATCTGCCAATGACCTTGAGGCCAACACCATTCTGGTGCAAATAATGGAGTC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCAAATAATGGAGTC
CATGACCGTGCCATTGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCAAACGGTGTGGAGGAAACATGG
GGAGGCTCAGCTTGGTCTAACAGCAGTGACTCAAGGGCTGTTGAAGCCACCAATTCTG
GGCAAACAATCCTACCCAGTGGATGATGTTCCCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTGTGCAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACATTGGCCGGTACTGGACAAAGCAGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCCCTAGGGAGCCCTAACAAAATTA
CATTGCTGGAACTAGAACATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATAACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAAGGTAGGCCGGCATGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACACCCGTCTCCACTAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGACTGGAGGTTGACCACTGCACCTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRILLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKGSLRGLYTTVDFGPADNMTKIF
TLLRKYEHPGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGKTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPPSPKMML
GPVTLLHVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWPYPQAPSGPTFSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTKQGPQQTLIVVPRFLLFPRGALNKITILLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCTTACATGTTAAAAAGCTTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTTAGTGACATTCCAGATGTCAAAAACGATTT
GCGTTCCCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAGAAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTCATG
CTGTCGGGGTGCCCAGTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGA
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCCTGGGTGTATTGCTAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACTGGAT
TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACCTGGAGTCACTTATTCTCTAACACAAGCTCGAACCTTACCAAGTGGCAGTATT
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATAACCCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAATGGGATTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTAAGTCATTCAATTCCTAACATTGTTTTAAATTGTTGTAACGGAT
AAAGGAAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPKEYSFEKVREESSFSDIPDVKNDF AFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDTLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLSLKKMMNVAEELQNCERIPHAIFSLSNLQELDLKS
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITS LP
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACCGCGTCCGGCCTCTCTGGACTTGACATTCCATTCTTTCATGACAAACTGACTTTTTTATTCT
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGGTTCTTCTCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTTGGGAGACCAACGTGG
GCTCAGTGCTTGCTGACTTATGCCTAGGTACATCGAAGTCCTTGACCTCCATACAGTATTATGCCTGTC
ATCGCTGGTGGTACCTGGCGCTTGCTGATAGTGTGCTGCTGTCTTACCTCAAAATACACAAC
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGTGGCTGAAAAAAATCACAAACCCAGACAAGGTGTGGTGGCCAAG
AACAGCCAGGCCAAACCAATTGCCACGGAGTCTTGTCTGCCCTGCACTGCTGTGAAAGGATATAGAATGTGTGCC
AGTTTGATTCCCTGCCACCTTGCTGTGCGACATAATGAGGGCTCTGAGTTAGGAAGGCTCCCTTCAGAAA
GCAGAGCCCTGAAAGACTTCAATGATGTCATGAGGCCACTGTTGTGATGTGCAAGAACAGAACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCCCTACTGTTGGGAATGCTGATAAACCAAGTCA
CACAGCTGCTTACACAAATCTACCCCTGCGTGGCTGGAACGTACGTTCCCTGGAGGTGTCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGCGTCTTAAGGCTGCCAGCGCTTGCAAAATGGAGCTGTA
AGAAGGCTCATGCCATTGACCCCTTTAATTCTCTGTTGGGGAGCTGACAATGGGGAGGCTGAAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC
AGTGAGAACTGCACTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTCTATGTCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAACATTAAAGCTTGTGACGGAACCTCCAGCAATGGCCTCTGCTAGGG
CAAGTCTGCAAGTAAACAGACTATGTCCTGTATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GAACAGCAAGAATTCAAAGAACTGTCCTTGCTTCTACTACTTCTCTCCTAACATCTTACATTCCAAACTGT
GGCGGTTACCTGGATACCTTGGAGGATCCTCACCAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGTCGACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTCAAAGAGATTTCTAGAAATAGAC
AAACAGTCAAATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTCTGCCCTGATTGGACAAGTCTGT
GGCGTGTGACTCCCACCTTCGAATCGTCAAACTCTGACTGCTGTGTTCTACAGATTATGCCAATTCT
TACCGGGGATTCTGCTTCTACACCTCAATTATGCAGAAAACATCAACACTACATCTTAACTTGTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACTCTAATGGAATAACTGCAACTAAA
GACCCAACTGCAAGACCAAAATTATCAAATGTTGGAATTCTGCTCTTAAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCATTACTCACCAATAATCACCTTCTGCACTCTCAACTTGTGAGTGTACCC
CGTCAGAAACAACTCCAGATTATGTGAAGTGTGAAATGGACATAATTCTACAGTGGAGATAATATAACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATAACACCCAGATGGCTTTTGAATCCAATTCA
TTTGAAGGAACTACTTGAAATCACCATTATATGTGGATTGAAACCAAACCTTTTGTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAATTGGTGGTTCTGATACCTGTAGAGCCTCTCCACCTGTACTTGTGATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCAGATGAAACTTGTAAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTTAATGCCCTTAAATTCTTGAGAAGTATGAGCTGTGATCTGAGTGTAAAGTTGATATGTGAT
AGCAGTGACCAACAGTCTCGCTGCAATCAAGGTTGTGCTCCAGAAGCAAACGAGACATTCTTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATCGAAGTGCAGTGGCAATTCAAGGATTACGCAT
GAAACACATGCCAGAAACTCCAAACCCAGCCTTCAACAGTGTGCACTCTGTTTCTCATGGTTCTAGCTG
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCAATTGTAAATCAACGGGAGACTACAAATACCAAGAGCTG
CAGAACTATTAACTAACAGGTCCAACCTAACAGTGAAGACATGTTCTCAGGATGCCAAAGGAATGCTACCTCGT
GGCTACACATATTATGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCATGTAAAAAAA

FIGURE 70

MELVRRLMPLLILSCLAEITMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTSLTCSSDRMVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDIIIGPIRLKRDRSASGNQFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCCGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG
GGACATCGGCCCGAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC
TGCTGCGCCGCCCGTGCCTGCCACAGCGCCACGCCAGCGCTTCGACCCCCACTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAGTCGGTAGCGAGTGGTCTGGTGGATTGGAAAAGGAAA
AGATACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAATTAAAAATTTTAATGCCAACAGTGGCAGATATTTCAAGGC
CTCTGGTGCCTAAATACATTGCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGGT
CAGAATATTCTGTGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTGGACTGTACTATTCCCTTTGA
ATGGTTTCACTCGCTTCCTGAGGATGAATCAGTCATTCCATAAGCGGCAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGATCAAACTGGAACAGCACAGGCTTCTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTTGCCA
CATAAATGGAAAAGTCATGACAATAGACAAACTGCTGGGGCTATAGGAGGGAAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGTCCTGGCTAAAAGTCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTACCCAGATGTGTTGACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGAGGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGTAAATGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATTGGCAGTTGCCACCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTCTACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTGTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTCTGCAACATCATAGAGTGTATTACAAAATCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATAACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATGGTGCACCTGTATAGGGCACTTACCGAACATGGAG
CTTACAGGACTGGAAGTGTCTGGGTGAGTCAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTCAATTATAAACTAAGTGTACTGTAACTTTACAAACGTTTAATT
TTTAAAACCTTTGGCTTTGTAATAACACTAGCTAAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVNTDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGWSLKVNGEAIYETYT
WRSQNNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

FIGURE 74

MARCFSLVLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCCTGACTTCACGATGG
CTCGCCCAACCTTAACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCACTGGATTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAACATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAGGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGAA
GGAGGCAATGCCGGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATAACCAGCGGCCAAGAAAATATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCTCCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAATGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTTGGTCAGTGTGTTACTGCTTATC
AGCTATTGACACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG
TTGACCTGCACAGCTTGGTAGACCTAGATTAACCTAACGTAAGATGCTGGGTATAGAA
CGCTAACGAAATTCCCCAACGGACTCTGCTTCCTAACGCCCTCTGGCTTCGGTTATGGTC
TTCATTAAGTATAAGCCTAACCTTGTGCTAGTCCTAACGGAGAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAAACCCCCCTATTGTGGGGATTGAGAACGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTTAGGACTTGGAGGAGAACCTCCGGACTTCAC
TAACCCCTCTGACATACTCCCCAACACCCAGTTGATGGCTTCCGTAAATAAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSPRLSRWLAQPYYLLSALLSAAFLLVRKLPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDI RMGLLYITLCIVFL
MTCKPPL YMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQS FAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNI PEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCGGTCACCCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCC
TTGCTCCTGCTGCCCGGCTCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCGAGGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGCCAGAGAGAAGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGAGAACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCATTGACGGCTGGAG
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGGGGGTGGTCTTCCCTTACCAAGTCCCCA
ACGGCGCTACCAAGTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCTTGAGCAGCTCTCCGGGCTGGAGGGAGGGCCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCATCATGTTGCCCGGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCCTGCACCGCTATGAT
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCGTGAGAACGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTCTTGCCGCTGGAAGTCCATGCCCTGGACCGCTGCACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTTACCCGCATCCTAAGTGGGCCCCAGAGCCTGGG
CCGAAGCTTGGCTTCCCCGACCCGCAGAGCCGCTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCGCCATTCCCTACTGGCTGTATTTATTGAGTGGTT
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCATTGCGGTTTGCGGCTTCTG
GAGGGTTCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTGGTGGGCCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTCTCCCTGCCCT
CACGCCTGGGGAAAGAAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTGTGAAGCCGTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTCCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCTCCCCGTTCC
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCCTGGCAA
AAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 78

MGLLLLVPLLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPLYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**GATGAT**GTGGCACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCAGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGCCGAGCTCGCGGTGGATCGGCACACGCAGCAGCGCA
CATACGGGACTCGGTGAGCGCGGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGGAGCTGCCAACGCCACCTATGCCACTACGCCCGGTGAAGAATTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGACGAGCGGCTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGCCACTCGAGAGGGAGCTGACAGCCTTCGCACCCCGAGG
AGTTCCCTCACATGCCGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGTGAGCAA
AGCGGAAATCCTGGGTAAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCGATGAGCTG**TGAG**CACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCGCTGTTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTCACACCCCCAACCCAGGGAGGGCTGTCAAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACACAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVAETLEDLDRNKGYVQVEEYIADLYSAEPGEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRILSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTGCCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCAGGGCGCGGGTGCAGGGATCCCTGACGCCCTGTCCCTGTTCTTGTCGCTCCAG
CCTGTCGTCGTCGTTGGCGCCCCCGCTCCCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCCGCCAGGCCCTCCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGTCGTCGTCGTCCTCTCTCCCTGCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCCGGGGCTCCGCACCCCTGGCCTGCCGCATTCTCCCTCTCCAG
GTGTGAGCAGCCTATCAGTACCAATGTCCGCAGCCTGGATCCCGCTCTGGCCTCGGTGTG
TGTCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGGCCCTCCATTGCTATCACATG
TTTACCAAGGGCTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGCTGCC
CTCTGAGGAATTCTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCCCTCAGTAGATGCCAATGCCATCCAGTCTCAAATGCTTTCTAGAT
GGCTGCTCTTCACAGTAACAAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACGTG
CAATAAAGATTGTAAGCAGACATTGCATTTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTTAATTTACAGAAGAATTGTTGGAAAAGTGGCTTAATGTTGGAAATTGAAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA
AAACTTACATCAGCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTCTTACCATGCCAACTGGTTGGCACCAACAAAATACGTAAA
GCCTCTGGTACAGAACGCTGTGCACTCATGAACAAATGATGTGCAAGAACCTGTTATAACT
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT
GATGCCATTCCCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTCACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGATT
CTCATATAACTGAAATGCTTACTGACATACTAGAACATCAGATACAAACTATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAAACCTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAACATTGATACTTAGACCAAAAAAA

0920000648 0324804

FIGURE 82

MSAAWIPALGLGVCLLLPGPAGSEGAAPIAITCFTRGLDIRKEADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMELFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCCGCACCGCGGCCGCCCACCGCGCCGCTCCGCATCTGCACCCGAGGCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTC
GGCGGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTGGGCCACCTGCTGTGCTGC
TGCTGGCGGGCGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGTCCAGTC
AAGCCCGGCCGGCTCTCAGTACCCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCA
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACTTACCTCCCAGCTAT
ACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGAGCAGAACGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTGCCAGCTTCCAGTACACCTGCCAGGCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCCTTCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTGGACCGATGCCCTGTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTGGCAGCTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCT
GCACTGCTGGAGGGAGAGATTTAGATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTT~~AGGC~~GTGGCTGACCAGGCTTCTCCTACA
TCTTCTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTGCTTGTCAATTGTTCAGC
TCCCCCAGGCTGTTCTCCAGGCTCACAGTCTGGCTTGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTTACACAGTGGCAG
ACAGCCGTTGTTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG
AGTCTCCCTCTGATTGGTTGGGGAAATGTGGAGAAGAGTGGCCCTGCTTGCAAAACATCAA
CCTGGAAAAATGCAACAAATGAATTTCACGCA~~G~~TCTTCCATGGCATAGGTAAGCTG
TGCCTCAGCTGTGCA~~G~~ATGAAATGTTCTGTCACCCTGCATTACATGTGTTATTCATCC
AGCAGTGTGCTCAGCTCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGT~~C~~ATTGTTCTCCTCGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCAT
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCCTGGTGCACCAA
AAGTGTCCCCAAAGGAAGGAGAATGGGATT~~TTT~~CTTGAGGCATGCACATCTGAATTAG
GTCAAACTAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGTCCTCTAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT
TGCATTAGTAAC~~TT~~GAAGGTATATGACTGAGCGTAGCATA~~AGG~~T~~TA~~ACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAA~~AA~~ACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGA~~A~~CTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATT~~C~~AGAGTTCTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCACFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLAGMNLRREISDYALEGLQSLSFYDNO
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPLSQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLA AHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCGCTGTTTGAAGAAGGTGAAGAACGTCGGACCCATGTGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCACATCAAGGTGATCAAGTTCATCCTCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGACTGCCGACCTTGAGAGGCCGACGGGCTACCGCACCTACCGCTGTGCCAACCC
CCTGGCCACACTCTCAAGATCCTGGCGCTCTTACATCAGGCTAGTCATCTTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAACGACTCGTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
CGACATCCCCGACGTCAGAACGACTTCGCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCCGCTTCCCTGTCGGAGGTGAGTGAGAACAAAGCTGCCAGCTGACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCGACGTGACCATCCGCC
CAGCATTGCCAGCTCACGGGCCCTCAAGGAGCTGTCCTTACACACAGCGGCCAAGATTGAAGGCCCTGCGCT
GCCCTTCTGCGCAGAACCTGCGGCCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGCGAGAACAAACCGCTACATCGTCATCGA
CGGGCTGCCGGAGCTCAAACGCCCTCAAGGTGCTGCCGCTCAAGAGCAACCTAACGCAAGCTGCCACAGGTGTCAC
AGATGTGGCGTGCACCTGCAAGAACGACTGTCCTCAACAAATGAGGGCACCAGCTCATCGTCTCAACAGCCTCAA
GAAGATGCCGAAACCTGACTGAGCTGGAGCTGATCCGCTGCCGACCTGGAGGCGATCCCCCCTCCATCTTCAGCCT
CCACAAACCTGCGAGGAGATTGACCTCAAGGACAACAAACCTCAAGGAGATCATCAGCTTCCAGCACCT
GCACCCGCTCACCTGCCCTAACGTCGTTACAACCAACATGCCCTACATCCCCATCCAGATGCCAACCTCACCAA
CCTGGAGGCCCTTACCTGAAACGCCAACAGATCGAGAACGATCCCCACCCAGCTCTTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCAAACAAACCTGAGCTTCCCTCCCTGCCGACATGCCCTCTGCAGAACCTCCAGAACCT
AGCCATCAGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCCGAGCTGCGGGCCCTGCACCT
GGGCAACAAACGTGCTGAGTCAGTCAGTCCAGGGTGGCGAGCTGACCAACCTGACGCGAGATCGAGCTGCCGG
CAACCGGCTGGAGTGCCTGCCGTGGAGCTGGCGAGTGCCCAGTGTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG
GCCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCCCTCAGGCCGGAGGGCAGGCCTAGCTTCTCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGCTGGCGAGCCTGGGGCCCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGGCCCTTTCTCCCTCTGAGACTCACGTCCCCAGGGCAAGTGTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGCTCCTCCCTGGAGGCCAGCTGCCAGGGCTGAG
CTGCCACCAGAGGTCTGGGACCCCTACTTGTCTGGTATTATTCTCCATCTCCACCTCCTTCTCATCC
AGATAACTTATACATTCCAAGAACGTCAGCCAGATGGAAGGTGTTCAGGGAAAGGTGGCTGCCCTTCCCC
TTGTCTTATTAGCGATGCCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCAACCG
CCATGGGACGGTCAACCAGCAGTGCCTGGCTGGCTCTGGTCCACGGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCCCTGGAGCTTGCCTCTTCAAGTTTTGTGGCAGTTTGTGTTTTTTTTTTAACTCAAA
AAACAATTTTTTAAAAAAAGCTTCAAAATGGATGGTTGGTATTAAAAAGAAAAAAAACCTAAAAAAA
AAAAGACACTAACGCCAGTCAAGTGGAGCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGGCCAGACGT
TGAACCTGTGTTCTTCCCTGGGGAGGGAGTTTTGTGTTTGTGTTTTGGGTTTTGGTGTCTGTGTTCTTCTCTCC
CTATTTGTTCTGGGAGGGAGTTTTGTGTTTGTGTTTTGGGTTTTGGTGTCTGTGTTCTTCTCTCC
ATGTGTCCTGGCAGGGCACTTCTGTCGGCTGTCGGCCAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGACCGTGCCTCACTGGCTGCAACCTGCCCTCTGCCCTGCCCTGCC
CGCACAGTGTAAAGGAGCCAAGAGGCCACTTCGCCAGACTTGTGTTCCCCACCTCTGCCATGGGTGTT
CCAGTGCCACCGCTGGCTCCGCTGTTCCATCAGCCCTGTCGCCACCTGGCTCTTCACTGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGGCTGGTCTCAAGCCGTTCCCGTCCCTGGCGC
CTGGAGTGCACACAGCCAGTGGCACCTGGCTGGAAGCCAACCTGCTTGTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCCCTAGATCAATCACGTGGACACTAACGGCACGTTAGAGTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCGCTCCATTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAATCCGTTACATGTGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAAAAAAAAAA

FIGURE 88

MRQTIKVIKFILIIICYTVYYVHNIKFVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNNNEWTLDKLQRQLTKNAQDKLELHLFMLSGLPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSQLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

CCCTGTTGCTGATGCTGCCGTGGTACTTGTCAATGGAGCTGGCACTGCGGCCTCTCCCCT
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGAACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTCAACTTGCAGGGGGT
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA
CGTCTACAATGGAGTCAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAAGCCAGCTCATGAATGCCCATCAGAAAGAA
GCTCAAAATTATTCCCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTGACATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCCCTG
GGTGGGAAACTGAAGTGGCCAGAAGCTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAACCTAAGATTTTAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLP~~LLL~~GLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTFGSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVSLSWGPYLYSMSLLEDKG~~L~~AEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVN~~F~~YNILTKSTPTSTM~~E~~SSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLK~~W~~KALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGD~~M~~ALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCA**CTCGGGCGTTGGCGTGGCA**
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTGAAACCTATA**AGTGACCTAGTGATCCCTCCGGGTGGATG**
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCAACCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCC**ATCTGTCTCCAG**
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCAGGAAGTCAGGTGCCATCATAACA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGGAGGATGCC**TGCTGGTGACTCAGGTGGACCCTT**
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCCGGTGTCTACACCAATATCAGCCACC**ACTTTGAGTGGATCCAGAAG**
CTGATGGCCAAGAGTGGCATGTCCAGGCCAGACCCCTCCTGCC**ACTACTCTTTCCCTCT**
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSCGPLACNKNG
LWYQIGVVSGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACCGCGTCCGGAGCGGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCAGCCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGCCCCGTGGCACCTGAGGAAGAGCTGAGTCACCTT
GCCCTGAGACAGCAGAAATGTGAAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCTCACACGGTGAAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCATATGTGGGAGGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCCTCTGTGATCCGTAAGCGATAACAACCTGACCTCACAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTCGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
CCCCTATGTCAACCACAGTGGGAGGCACATCCTCCAGGAACCTTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGCCCTCATACCAGGAG
GAAGCTGTAACGAAGTCCCTGAGCTCTAGCCCCACCTGCCACCATTCACTTCAATGC
CAGTGGCGGTGCCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGTGGTCAGCAACA
GAGTGCCCATTCCATGGGTGTCGGAACCTCGCCCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTGGCTTCTCAACCCAAG
GCTTACAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCAGCTTGCTGAAGACTCTACTCAACCCCTGACCTTCTATC

AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGTGAAA
TGCTGTGAGCTTGACTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCTTAGATTCCATCAAATAAGATGCTGTAACTAGCATTTTGATGCTCTCCCTCCGC

ATCTCATCTTCTCTTTCAATCAGGTTTCAAAGGGTTGTATACAGACTCTGTGCACTA

TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT

TTCCTACCTGACATCCAGAAACAATGGCCTCCAGTGCATACTCTCAATTTGCTTATG

GCCTTCCATCATAGTGCCCACTCCCTCCTTACTTAGCTTCCAGGTCTTAACTTCTCTG

ACTACTCTTGCTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCAATTGC

TCCATTGAGATTTTGCTTCTCAGTTACTCATTGTCCTGGAAACAAATCACTGACA

TCTACAACCATTACCATCTCAACTAAATAAGACTTTCTATCCAATAATGATTGATAACCTCAAA

TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVALVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTEHVVRSPHPYQLPQALAPHVDFVGGHLRFPPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYN LTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLM SAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHECLDEEVEGQGFCSGPWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCCGGGCCACACCTGTCTGAGCGCGCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTTCCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATAACCGCCTCCCTGCGTCTGCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTCAAGGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAAGCAGTGCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCAGCCATGCCAGCAGATGAA
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGCCAGGGTCTGGGTCTAT
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCCTACCAAGCAATGCAGTGCCTGCCAGCCAGGGGCCAGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAATTATTGGATTTTCAGG
GCACCAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTCCTGGCAGCAATTAAGGTCTTCATGTTCTATTAGGAGAGGCC
AAATTGTTTTGTCATTGGCGTGCACACGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAATACTGATTGGGCAATGAGGAATATTGACAATTAAAGTTAATCTCACGTTTG
CAAACTTGATTTATTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQPSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA
AHCIHDGKTYVK
TQKLRVGFLKPKFKDGGRGANDSTSAMP
EQMKFQWIRVKRTHVPKGWI
KGANDIGMDYDYA
LLELKPKH
RKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKROQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPL
KYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGGTCTCTCGAGCCTGCTGCCGCCCCACCAAGCCATGGTGGTT
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTTCACCTCCCTGCTGCTGCTG
GCGTGCACAGCCATCCTCAATGCCGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGCTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGTCCCAGAAGGTGGGTGTTGCCTGGTGAGC
CCCACCCCTGTGTATTCCCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCTGGGTGGAGAAGATCGTGAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCCGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGGCGGGCCTCGGGCGTTTCCCCCGCTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCGCCAACGGCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTATATAATGTTAATGATTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTCTCCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCCGTATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGCCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGAGAAATCTGTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACGTCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTGGACCCCAAGATGTCCTGACAGGGCAAG
GGAACCTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCCTGGCTCTGCAGTCGCTTGCAGGTGAGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTGAATGGATAACCAACTCAAAGGG
TGAAGAGGTCAAGCTGTCTCCTGTCACTCTCCCCACCCCTGTCCCCAGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCCTCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTGCCCTCCCTGGTGTGGCTGAGTCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCCTACCTGGCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGGCCACTGGAGTGGGTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAA

FIGURE 100

MHGSCSFLMLLPLLLL VATTGPVGALTDEEKRLMVELHNL YRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKR PYQEGETPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGI PAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTVPSPRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTAGCAGGCTTTCAATTGGGAAGCCCCCTAACAGAACCGTCAATTCCAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTCTGCTTGCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAGTTCATGAGCCACCTCAAAGCCTCGAGAAGTGAACACTGAACAAACATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCTCGGCAAATATTACACTTCTCCTTGCTGGAAACAGGATTGAAACTCCCTGA
ACATCTGAAAGAGTTCAGTCCCTGAAACTTTGACCTTAGCAGCAACAATATTCAAGGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA
TTTGGCCAACACACACTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTCGAATTGAACCGAAACAAAGATTAACAGGTTAGATGGACTGACATTCCAAGGCCCTGG
TGCTCTGAAAGTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGATGGACTTTGGGGCTGAGCAA
CATGGAAATTTCAGCTGGACCAATAACACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCAGCCAAATGCCATCACAGGATCAGCCCTGATGCCAGGGACTCTGCCAGAAAGCTCAG
TGAGCTGGACCTAATTCAACTCAAGGTTAGATGATGATCAAGCTTCTGGCCTAAGCTTAAACTAAAC
ACTGCACATTGGAAACACAGAGTCAGCTACATTGCTGATTGCTCAGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACAAATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAACAGCCTTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGAACGCAATCATGCTTCAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATT
GCATTAAATACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAACCT
TCAGAGCTTGTAAATGCCAGTTGTGCTCAGCTGCCAGCAGTGAATTCCCAATGACTTTGCTTGGAAAAAGACAATGA
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGTGAATTCCCAATGACTTTGCTTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAACGGTGGCGAGGTGATGGAGTATACCAC
CATCCTCGGCTGGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAACTTTGGTTC
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCCT
CCGAGCTGGGGCATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCTGGCAGAAGGA
TGGGGGACAGACTCCAGCTGCACGGAGAGACGCATGATGATGCCAGGGATGACGTGTTCTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGACAGCTCAGAACAGTGCAGGAAGTATTCAAGCAAATGC
AACTCTGACTGTCTAGAAACACCATCATTGGGCCACTGTTGGACCGAACGTGTAACCAAGGGAGAAACAGC
CGTCTACAGTGCATTGCTGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAAGATGATAGCCCATTGGTGGT
AAACCGAGAGGACTTTTGAGCAGGCAATCAGCTCTGATATTGTGACTCAGATGTCAGTGTGCTGGGAA
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGAGGAAACGTCGGCCACTGTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGTGTGTCATAGC
CGTGGTTTGCTGTGGTGGCACGTACTCGTGTGGTGGTCACTCATATACACACAAGGGGAGGAATGAAGA
TTGAGCATTACAAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCATCTCAGGGACGTT
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAACGCCACCCAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACCCACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC
CACAGATCTGTTCTTGTCCGTTGGATCCACAGGCCATGTATTGAAAGGGAAATGTGTATGGCTCAGA
TCCTTTGAAACATATCATAACAGGTTGCACTGCTGACCCAAAGAACAGTTAAATGGACCAACTATGAGCCCAGTTA
CATAAAGAAAAAGGAGTGTACCCATGTTCTCATCTTCAGAAGAACCTCGCAACGGAGCTTCAGTAATATATC
GTGGCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAAATGAAGGACTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTGTGAAATCCAGAGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATTCTCCAGACTTGGACTCTGGTCAGAGGAAGATGGGAAAGAAAGGAC
AGATTTCAAGGAAGAAAATCACATTGACCTTTAACAGACTTTAGAAAACAGACTCCAAATTTCAGTC
TTATGACTTGGACACATAGACTGAAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTATTAA
AAAGAGAGAGAAATCTTATGTTTTAAATGGAGTTATGAAATTAAAGGATAAAATGCTTATTATACAGAT
GAACCAAATTACAAAAAGTTATGAAATTAAATGATATAAGAACACCTTTAAACT
TTTTTTAACTTGTGTTATGCAAAAAGTATCTTACGTAATTAAATGATATAATGATTATTATGTATT
TTATAATGCCAGATTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCTGTACCATTT
TTAAATAGAAGTTACTCATTATATTGACATTATAATTAAATAAAATGTGTCATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRSLFIKASSMSHLQSLREVKLNNELETIPNLGPVSAN
ITLLSLAGNRIEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRISSAIPPKMFKLPQLQHLELRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLSRLDDSSFLGLSLLNLHIGNNRVSYIADCAFRLSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNFSFVNASCAPQLLKGRSIFAVSPDGTVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDPMTFAWKKDNELLHDAEMENYAHLLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCQAQN
SAGSI SANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPPLNWTKDDSPVTER
HFFAAGNQLLIIVSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLDDG
WATVGVIIIAVCCVVGTSLVWVIIYHTRRRNEDCSITNTDETNLPADIPSYLSQGTTLAD
RQDGYVSSESQSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTCSPDPRTVLMHYEPSYIKKKECYPCHPSEESERSFSNISW
PSHVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG
AAGGATGCAGGACCGCAGCTTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGACACAGGGAGCATTAAGAACGAAATGAAA
TAAACCAAGAGTAGACCCCGGGGGTTGGTGTGTTCTGACATAAAATAATCTTAAGCAGCTGTTCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCATTTTCTC
TATAAAGGAGAAAGTGGCCAAAGGAGATAAAGGGATGAAAGTGGGGCTTTTAGTAAAGTAAAGAAC
GGTGTGGTGGCTTTCTTCTTTGCAATTCCCACAAAGAGGAGAGGAAATTAAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTGGCCGGCAGATTGAGGCATTGGGGAGAGAACCCAGCAGAGCACAGTTGGA
TTTGTGCCATGTGACTAAATTGACGGATAATTGAGCTGGATTCTTCATCAACCTCCTTTTAAAT
TTTATCTCTTTGGTATCAAGATCATGCGTTCTCTGTCTTAACCAACCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACAGGACCAACACCAGATAAAATTATGA**ATGTTGAA**CAGAT
GACCTTACATCCACAGCAGATAATGATAGGCTCTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGC
GCTGGCTCTTCAACTCTGTGGTGGCTGGTCTGGTGGCCCTCAGACCTGCCCTCTGTGTGCTCTGAGCAA
CCAGTTCAGCAAGGTGATTGTGTTGGAAAAACCTCGCTGAGGTTCCGGATGGCATCTCCACCAACACAGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTGAGGCACTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGGAACCTAACACTCTGGA
ACTCTTGACAATCGTCTTACCATCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTTATGCTTTAACAGAAATTCTCTTGGCCGACTAGACTTAGG
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCTTGAAGGTCTGCCAACCTGAGGTATTGAAACCTG
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCCCAGAT
TCAAGTGAACGGAATGCCTTGACAACCTCAGTCACTAGTGGAGATCAACCTGGCACACAATACTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTGATCATCTAGAGCGGATACATTACATCACACCCCTGGAACTG
TAACGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCGGTG
TAACACTCCCTCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGAAATTACTCACATGCTATGCTCCGGT
GATTGGAGCCCCCTGCAGACCTCAATGCACTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCTACAAAGTGGGATAGCTGT
GCTCAGTGATGGTACGTTAAATTCTCAGGATGAGGACCCAGACAGATAACATGTGGTGGTGGTGGTAA
TTCCGGTGGGAAATACTACTGCTTCAGCCACCTGAAATGTTACTGCAAGACATGGGGCTACAAAGTGGGCTCCACCT
AACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGACCCAGACAGATAACATGTGGGCTCCACCT
AGTGGTCAGTGGAGACCAATGTGACCCCTCTCACACCCACAGAGCACAAGGTCGACAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGATCCCAGGAATTGATGAGGTCTGAGACTACCAAAATCATCAT
TGGGTGTTCTG GCCATCAACTCATGGCTGAGTGTGCTGGTCAATTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAATGTGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCATGCTATCGAGCATGAGCACCTAAACTATAACTCATACAAATCTCCCT
CAACCCACACAACAGTTAACACAATAAATTCAATACACAGTTCACTGCAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTGAGTTACAAAAAACAAATCAAAAAAA
GACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTATTAAATTCTATTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQQLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFNDNRLTTIPNGAFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAAATTTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVWDWETTNVTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIIINVDEITGDTPMESHPMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS
VHEPLLIRMMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRNLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSNIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELRNKKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNNEIS
WTIEDMNGAFSGLDKLRRRLLQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQCLKWLPQWVAENNQOSFVNASCAPQLLKGRSIFAVSPDGVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDSELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGECVLQCIAGGSPPPKNWTKDDSPLVVTERHF
FAAGNQLLIIVSDVDSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLLLDWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTIADRO
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDPFETYHTGCSPDPRTVLMHDHYEPSYIKKKECYPCHSEESCERSFSNISWPS
HVRKLLNTSYSNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCCAGCTTGACTTGAATGAAAGGAGCCCGAGCCCCGGAGCGCAGCTGAGAC
TGGGGAGCGCGTCGGCCTGTGGGCGCCGCTCGCGCCGGGGCGCAGCAGGGAAAGGGGAAGCTGTGGCTGCC
CTGCTCCACGAGGCAGCCACTGGTGTGAACCGGGAGAGCCCTGGTGGTCCGTCCCTATCCCTCTTATATA
GAAACCTTCCACACTGGGAAGGAGCAGCGGAGGAGGCTCATGGTAGCAAGGAGGCCGCTGATCTGCAG
GCGCACAGCATTCCGAGTTACAGATTTACAGATACCAAATGGAAGGCAGGAGGCAGAACAGCCTGCC
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGCACCCCTGCAGGACCATGCCAGAGCCGGTGCTGC
TGCTCCCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCGTGAGGGCCCAAGGATTGGCGAA
GTGGCGGCCACAGCCTGAGCCCGAAGAGAACGAATTGCGGAGGAGGAGCCGGTGCTGGTACTGAGCCCTGAGG
AGCCCGGGCTGGCCAGCCCGGTCAAGCTGCCCGAGACTGTGCTGTTCCCAGGAGGGCGTCGTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCGTGAGCACACCAACCACCTATCTCTGCAGAACACCAGC
TGGAAAAGATCTACCTCTGGAGAGCTCCCGGCTGCACCCGGCTGGAGACACTGAACCTGCAAAACAACCAGC
CTTCCCCAGGGCTCCAGAGAACGGCGTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCAATAAACAGC
TGACCTTGGCACCCCGCTTCCGTGAAACAGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT
ATGGGCTCACCTTGGCCAGAACGCAAACATTGAGGTCTGTGACCTGCACAAACAACAGCTGGCAGACGCCGGC
TGCCGGACAACATGTTAACGGCTCCAGAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGGCT
TCAGCGAGCTGAGCAGCCTGCGGAGCTATACTGAGAACAAACTACCTGACTGACCGAGGGCTGGACAAACGAGA
CCTTCTGGAAGCTCCAGCTGGAGTACCTGGATCTGTCCAGCAACAACTGTCTGGGTCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGAGCGGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGTCACAGAACCCAGCTGCCAGCAGGGCATCCACCCACTTGGCTTCCAGGGCC
TCAAGGGTTGCACACGGTGCACCTGTACAACAAACAGCCTGGAGCGCTGCCAGTGGCTGCCCTGCGCGTGC
GCACCCCTCATGATCCTGCACAAACAGATCACAGGATTGGCCCGAAGACTTGGCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACAGGCCACAGGTGACCGCCTCCGCAAGCTGCCCTGCTGC
GCTCGCTGGACCTGTCGGCAACCGGCTGCACACGCTGCCACCTGGCTGCCCTGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCCTGGCACGGGGCTGGCGGATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTCGCAGCCAGGCCCTGGCCCGTGCCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCGAGGGCTCCCGAGTCACCTGAGTACCTGTACCTGCAGAACACA
AGATTAGTGCCTGGTCCCCGCAATGCCCTCGACTCCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAGC
TGGCTGGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTGACATTCCAAGGACGGTGGCCCTGGGGAGGAAAAGGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAAGATAGTGACAAGGTGATGCAAGATGTGACCTAGGATGATGGACCGCCGGACTTTCTGC
AGCACACGCCCTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGAACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGCTGACAGCTCATATCCCCACCCCTCCACGGCGTGTCCACGCCAGAACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACAACTACCCCTCAAACCAACACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAGGGCTGCCCTGCCACACACAGGCCAACACAGGCA
TCCCCTCCCCCTGTCGACATGTGATGCTATGCATACACACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAAGCTATGCCACAGACAGCTTGGCCAGCCAGAATGCCATAGCAGCTGCCGTGTGCCCT
GTCCATCTGTCGCCGTCCGTTCCCTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCCACCCCTCT
GGAACTCACAAAGCTGGCTTTATTCCCTTCCATCCATGGGGACAGGAGCCTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCAGGTGCTGGCAGTCACCTGCTAAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACCTTCCAATGGCAAGCCCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGACA
CAGGAGTGAAGCAGAGGTGATGGGGCTGGCTGAGGCCAGGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGACA
GTTCTTCAGGCCTGTGGGGAGTTCCGGGTGCCCTTATTCTTATTCTTAAGGAAAAAAATGATAAAAAT
CTCAAAGCTGATTTCTGTATAGAAAAACTAATATAAAAGCATTATCCCTATGCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAEEEPLVLSPEEPGPGPAAVSCP RDACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNOLEKIYPEELSRLHRLETLNLQNNRLTSRGLPEKA FEHTNLNYLYLANNK
LT LAPRFLPNALISVDFAANYLT KIYGLTFGQKP NLR SVYLHNNKLADAGLPDNMFNGSSNV
EV LILSSNFLRHPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ET FWKLSSLEYLDLSSNNL S RVPAGLPRSLVLLHLEKNAIR SVDANVLPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITS PQVHRDAFRKLRLLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEAALA
RGALAGMAQLRELYL TSNRLRSRALG PRAWVDLAHLQ LLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANA FDSTPNLK GIFLRFNKLAVGSVVDSA FRRKLHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGCGCCGCAGCAGACCTGCTCCGGCGCCCTGCCGCTGTCCTCCGGAGCGGCAG
CAGTAGCCCGGGCGAGGGCTGGGGTTCCCTCGAGACTCTCAGAGGGCGCCATCGGCCACCACCC
CAACCTGTTCCCTCGCGCGCACTGCGCTGCCAGGACCCGCTGCCAACATGGATTCTCTGGCTGGT
GCTGGTATCCTCGCTACCTGCAGGGCCGCGAGTCAGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTATGGTGGAGGATTGACTGCTGCTGGGCTGCCAGTCTGGGACAGTGTACAGC
TGTGCCAACACGATGCAAACATGGTAATGTATCGGCCAAACAAGTCAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGTAAGCACAGGTGATGAACACTTA
CGGCAGCTACAAGTGTACTGTCATGCAACGGATATACTGCTCATGCCGATGGTCTGTCAGTGCCCTGACCTG
CTCCATGGCAAACGTCAGTATGGCTGTGATGTTAAAGGACAAATACGGTGCCAGTGCCTCCATCCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGATGAGTGTGATGAAATGTGCTACAGGAAGAGCCTCTGCCCTAGATT
TAGGCAATGTGTCACACTTTGGGAGCTACATCTGCAAGTGTCAAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCATGACATAGACGAATGCTACTTGGTCAGTCACTGCAAGCAGCTTGCTCGATGTTATAA
CGTACGTGGGTCTACAAGTCAAATGTAAGAAGGATACCGGTGATGGACTGACTGTGTTATATCCAAA
AGTTATGATTGAAACCTTCAGGTCAAATTGTCATGACAAAGGAAATGGTACCTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGAGTACTTGGTGGCCTCGGAAGACACCATATACTCTCTATCATTACCAA
CAGGCCTACTCTAAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATCCTACTCCACCAACCACCC
CCTGCCAACAGAGCTCAGAACACCTCTACCCACCTACAACCCAGAAAGGCCAACACCAGACTGACAACATATAGC
ACCAGCTGCCAGTACACCTCAGGAGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGAGG
AGATGTTGTTCACTGTTCTGGTACACAGTTGTAATTGACCATGGACTTGTGGATGGACTGAGGAGAAAGACAA
TGACTTGCACTGGGACCAATCAGGGACCCAGCAGGTGGACAATATCTGACACTGTCGGCAGCCAAGCCCCAGG
GGGAAAAGCTGCACGCTGGTGTACCTCTCGGCCCTCATGCATTAGGGACCTGTGCCCTGTCATTCAAGGCA
CAAGGTGACGGGGCTGCACTGGCACACTCCAGGTGTTGTGAGAAAACACGGTCCCCACGGAGCAGCCCTGTG
GGGAAGAAAATGGTGGCATGGCTGGAGGCAAACACAGATCACCTGCGAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAATTAAAGGAACACTGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCAATTGATGGTTTCAAGTATATGAAGGGTGGCACAGAGAGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GGCCATTGTTAGAATACTTCATAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAAAATTAGA
AAAAAATTGTCATTAAAGATGGTTAAAGATGGTTCTTACCAAGGAAAGTAACAAATTATAGAATTCCCAA
AGATGTTTGATCCTACTAGTAGTATGCACTGAAATCTTACAAGTAAATAATTGGACAAGGCTTAATTAGG
CATTCCCTCTGACCTCTTAATGGAGAGGGATTGAAAGGGGAAGGCCACCAATGTCAGCTACTGAAATA
TCTCTCCCTTATGCACTCAGTATTAAAGAAAAAGGAAACTATTATTCCAAATGAGAGTATGATGGAC
AGATATTGTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTCATGGATGATGTTCAAGATTTTTTTAAGAGATCCTCAAGGAACACAGTTCAGAGAG
ATTTCATGGGTGCACTCTCTGCTTCGTGTCAGTATCTGGCTGCTGAGAAAGAGTGCCCTGCC
ACACCGGCAGACCTTCCTCACCTCATCAGTATGATTCACTGCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTGGTAAACATAGGTACAATAGAAGGTCTCTGTCAATTAACTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAATCATTAAAGCCTTGAGTAACGGCAGAAATATGGCTGTAGATCCATTAAATGGTTCATT
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTTCAGTTGATGCCAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCAAAGTACTGTATAACATCTGTTATTATTTAATGTTT
CTAAAATAAAATGTTAGTGGTTTCCAAATGGCTAATAAAAACAATTATTTGAAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGDVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYI PPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPAASSTPPGGITVDN
RVQTDPQKPRGDVF SVLVHSCNFHDHGLCGWI REKDNDLHWEPIRD PAGGQYLT VSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGLQVFVRKHGAHGAALWGRNGGHGWQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAGGATTACACCGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACCTTCCTTCCTTGCAACAGGTGCTTGCTCGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTCACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA
ACAATGCCAAATACTTAAGTCTGTGAATAAGTCTGTGGTCCTGACTTGGAAATACC
AACACAAGTCACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACCTATCTGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGGAGGAACCTGTCAGTGAATGGAAAGTGAATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAACAGAACATGGACTATGTGTGCTGTGCTTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATGTACACCTTAGCAAGTATAACTGGAATATCACTATTGATT
ATATCCATGTGCTTCTTCCTATGGAAAAAAATCAACCCATCAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTCAGCCTCTGATTGTATCGGGCAAGATTGACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCCAGAGT**GAAC**TTTCAATGG
GCTAAACAGTACATTGAGTGAAGAAATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATCCTTACA
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGAAATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGCACAGGGTTCTCATAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCAACACTGAGACTATCCTGTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTTCCAATTCTATCTTGTATTGTACAA
CAAAGTAATAAGGATGGTGTCAAAAAACAAAACATGCCTCTCTTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGCTTTAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNVSPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPTEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGC~~AAATGGCGCCCTCCGGGAGTCTTGCA~~GTCCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGCCTCCCTGGACGCACGGCGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATA~~GAATT~~TATGCCCGTGGTGCCTGCT
TGTAAAATCTCAACCGGAATGGAAAGTTGCTGAATGGGAGAAGATCTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTATAAGT~~GATAAAGAGTGG~~AAGAGTATTGAGCCC~~TTT~~CATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAAT
TATTATCAGAACCTGACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGACTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAAGACAACGCTCTGGGTCCATCATTGCCACAGATAAATCCTAGTTAAATTATAG
TTATCTTAATATTATGATTTGATAAAAACAGAACGATTGATCATTGTTGTTGAAGTG
AACTGTGACTTTTGAAATATTGCAAGGTTCACTGTTAGATTGTCTTAAATTGAAGAGTCTA
CATTCAAGAACATAAAAGCACTAGGTATACAGTTGAAATATGATTAAGCACAGTATGATG
GTTTAAATAGTCTCTAATTTGAAAATCGTCCAAGCAATAAGATTATGTATATTGT
TTAATAATAACCTATTCAGTCTGAGTTGAAAATTACATTCCAAGTATTGCAATTAT
TGAGGTATTAAAGAAGATTATTTAGAGAAAATATTCTCATTGATATAATTTCCTCTG
TTTCACTGTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTTTCAGTGACAATTCTGGTCTTTAGAGGTATATTCAAATTTCTCTG
ATTTTAGGTTATGCAACTAATAAAACTACCTTACATTAAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTAAGTTCATGGTATTCTCTGATT
CAACAAAGTTGATTCTCTGTATTCTTACTATGGTACATTTTATT
CAAATTGGATGATAATTCTGGAAACATTTTATGTTTAGTAAACAGTATTGTT
GTTTCAAACGTGAAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGAATTAAAATT
TTGGCCACTTTTCAGATTTACATCATTCTGCTGA~~ACT~~CAACTGAAATTGTTTT
TTTCTTTGGATGTGAAGGTGAACATTCTGATTGTTCTGATGTGAAAAAGCCTGGTA
TTTACATTGAAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAAG
CATCTCTGTATATGCTTAAATGTATTGTCCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAAATAACATTATTATTTTAAAGACAA
ACTTCATATTATCCTGTTCTTCTGACTGGTAATTGTGTGGGATTTCACAGGTAAA
GTCAGTAGGATGGAACATTAGTGTATTCTTACTCCTTAAAGAGCTAGAACATACATAGTTT
CACCTTAAAGAAGGGGGAAAATCATAAATACAATGAATCAACTGACCATTACGTAGAC
AATTCTGTAATGTCCCCTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATCGTAATATACAAGTTCTTAAAGCCTCTCCTTAAAGTAAATATTGTACCATT
AAAGAGTTGGATGTGTAATTGTGATGCCCTAGAAAATATCCTAACGACAAAATAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

CGAGTGTCCAGCTGCGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTGCTAACCCAGTGGACAGGCAGGATTGGAAGAGCGGG
AAGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTGGTCTGAGCTGTGCAAGGCCAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATAAAGAGCTGGGCAACAAAATGGAAGCCTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCGTGAAATGCCAACAAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCCTGGAGGACCTTGCCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCAGCAGTTCTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAACGCCGTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGAACTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTGGGTGATCTGCACCGTGCCTGGAGCTCACCGCCCTGCTC
TCCCTGACCAAGCCACGAACGAGCTGGAGGGAAATCTGCGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGTCGTGGG
GAGGGTGTCAAACGTACACCCCGTAGACAGAAGAGGTTCTGTAGGTACCAACATGGCAA
CAGGGCCCCACAGCTGCTATTGCCCCCTCAAAAGAGGAGGACGAGTGGACAGCCGCACA
TCGTCAGGTACTACGATGTCATGTCATGAGGAAATCGAGAGGATCAAGGAGATCGAAAAA
CCTAAACTTGACGAGGCCACCGTCTGTGATCCAAAGACAGGAGTCCTCACTGTCGCCAGCTA
CCGGGTTCCAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAAATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCATTGACTTCTCTAGGCACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAACGCTG
GTGGTGCACCCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACACCTCTTGCAGGGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCCTGCC
TGTGCTTGTGGCTGCAAGTGGCTCCAAATAAGTGGTCCATGAACGGAGCACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTCTGTCCTTCCCCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCCCTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTGAGCCTGTGCCATCCCTGGCCCCAAGGGTAGGATCA
AAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGGTGTGAGATGTTCAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCTACCAAGAAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEELPGTKYQAMLSVDDCFGMGRSAYNEGYYHTV
LWMEQVLKQLDAAGEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDFYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYVGQQYEPHFDFSR
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATFPDLGAAIWPKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTTTAGTGGAAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT
TTCATTATTACCGTTTGGCTGGGGTTAGTTCGGACACCTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGATGCTGGCTGGAAAGCCAGGGCCTGCTCTGCTCTGGCTCATTGACCC
CAGGTTCTCTGGTAAAAGCTGAAAGCCTACTACTGGCCTGGTCCCCTCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCAACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGTGAGCCTGAGCCTCCCTGCGGGTTCCCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTCAGGGCTGTAGGGGAGCGAGGAGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGATTGTCCTACTACAGGGACCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCGTGAGCGGGTGTGGCTGACCTCCGAGCTACACTGTCCA
CTTGGCGTGGCTGTGAACCGTACGGTGGCCCATCACTCCCTCGTTACTCTACTTCAGTGGCAGCGGGGG
CCCAGGCTCCAGCAGGGATGAGGTGGTCTCATGGGATGAGCGGCCGCTGGCTATGTCAGAGACCTGC
GCCACCTCACACACACTTGGGCCACTACGACTGGTTCTCATCATGAGGATGACACATATGTGAGGCC
CCCGCTGGCAGCCCTGCTGGCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTCATG
GCGCAGGCGAGCAGGCCGGTACTGTATGGGCTTGGTACCTGTTGTCACGGAGTCTCTGCTTGTCTGC
GGCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGGCCCTGACGAGTGGCTGGACGCTGCCTCATG
ACTCTCTGGGCTGGCTGTCACAGCAGGGGAGCAGTATGCTCATTGAACTGGCAAAATAGGG
ACCCCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGGCTTGGCTGACCCCTGCTCCGAAGGTACCCCTCATG
ACCGGCTCCACAAACGCTTCCAGCGCTTGGAGGCGGGCTTACAGTGAAATAGAACAACTGAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACCACACTCTGCTTGGACTACTTCACAGAGCAGCACACCTCTCTGTGAGATGGGG
CTCCAAGTGGCCACTACAGGGGCTAGCAGGGAGCTGGTATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGGCTATCAGCCCCGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGCGCTTCGACCCAGCAC
GGGGCATGGAGTACACCCCTGGACCTGCTTGGAAATGTTGACACAGCGTGGGACCCGGGGCTGGCTCGCA
GGTCAGCCTGCTGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGTCAGGAGCAGGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTCTCGAGGGGTTGAGCCAATGTCC
TGGAGCCACGAGAACATGCTCACCTGTTGGTCTACGGGCCAGAGAAGGTGGCCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGAGCAGCGGAGTTAGAGCGACGGTACCGTGGACAGGCTGGACACTCT
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCAGGACTCTGGCTCG
TCTTCCCTACCAACCGTGTGGACAAGGCCCTGGCCGAAGTCTCAACCGCTGTCAGTAATGCCATCTGGCT
GGCAGGGCTTCTCCAGTCCATTCCAGGAGTTCAATCCTGCCCTGTCACCACAGAGATACCCCCAGGGCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCGGGGGGCTCTATAGGGGGGAGATTG
ACCCGGCAGGCTCTCGGGAGGGCTGCTTCAACAGCTGACTACCTGGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTTCCCTGGTCTCAGGGCTCC
ACCTTTGGCGCTAGAGCCAGGGCTGGTGTGAGAAGTTCTCCCTGCGAGACTGCAAGCCACGGCTCAGTGAAG
AACTCTACCAACCGCTGCCCTGAGCAACCTGGAGGGCTAGGGGGCGTGGCCAGCTGGTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCTGGGGCCCTAACCTCATACCTTCCCTGTGCTGCCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQQVSHGDERPAWLMSETLRHLHTHGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLOQASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTL DLLECVTQRGHRRALARRVSSLRPLSRVEILPMPYVTEATRVQLVPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKA AAAAEERRYPG
TRLAWLAVRAEAPSQVRLMDVSVSKHPVDTLFFLTWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPGADPSRGAPIGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~G~~CCAACGTGAGAGGAACCGTGCGCGCTGC~~G~~CTTCCTGTCCCCAAGCC
GTTCTAGACGCGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTGG
AAGCATTTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCC~~T~~TGATAAGTATAGAGACCAATACA~~A~~CTG
GTTCTCCTGCACGCC~~C~~ACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTTAA
AAAAGGATCCATCACAGC~~C~~TTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT
CAATATCCCAGAAAAGTGT~~C~~CTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGC~~C~~TGAAATATGCTGGAGTATTG~~C~~AGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAACCAAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTT~~C~~AGATATGGCTGTTACTTTAATGGACTGACTCAA
ATCAGATGCATGTGATGATGTATGGGTATACCGC~~T~~TAGGCATTGGCATTGGCATATTTC~~A~~AT
GATGCATTGGTTTCTTACCTCCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTCATTATTG~~T~~AGTAGTA~~A~~CTACATATCCAA
TACAGCTGTATGTTCTTTCTTTCTAATTGGTGGC~~A~~TGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGAAATG
TGTGGAAAGAAGTGT~~T~~TAAGAATAATAATTGCAAATAACTATTAAATAATATTAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTGCTGATTGGTT
AAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAA~~A~~CTTTAGCTGTGTGTTCCCTTACTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTTCTCAAATGTACAACTAAGCAACTAAAGAAA
ATTAAGTGAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMRK
AYKYAFDKYRQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCACCGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGGATGCTTCTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTGCCTGTTCATCACAGATGTGTTGACATTCGCAT
CTTCAAAACCTGTGATGAGAAAAGTTCAGCTACCTGAGAATTTCACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAAGAATTGTTGCCATTGAACGGAAATTCAATCC
AGCTGCTACTTCTTTCTACTGACACCATTCCCTGGCGTTAACGTTAAAGAAACTGCTCAGC
CATGGGGGCTCACCTGGGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTACAAGA
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTGGATTGTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAAATCTCTTTAAGAACAGAACGGACAACTCAAATGTGAAAGAACAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAAATAAGTAGTTAAATGTTAAAAAAAAAAAA
AAA
AAAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGS

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCCGCCTGCCGCTGGCCCCTCAGCAACCCTGACATGGCGCTGAGGCGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTCTGCTGCTTTTCAGGGGCTGCCGTAGAGGGCTGTAATC
TCAAATCCAGCAATCGAACCCCCAGTGGTACAGGAATTGAAAGTGTGGAACACTGTCITGCATCATACGGATTGCG
AGACAAGTGACCCAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCTGAGAAATACTGGGAAGACATCCCTGAAGATCTGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGAACCCCTGCTGTAGAGTGCAGGCTGTACCACTAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGATGACCACTGCCACGGATT
CCAGAGCCAATCCAGATTGCAATTCTCTTCACTTAAACTCTGAACACAGGACTTGGTGTCACTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTTGCTCTGCTGTACTGCCCTGA
TCACGTTGGCATTGCTGTGCTACAGACGTGGTACTTCATCAACAATAACAGGATGGAGAGAAAGTTACAAGA
ACCCAGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGGCAGCTCAGACACAAGTCATCGTTG
TGATCTGAGACCCGGGTGCTGAGAGCGCACAGAGCGCACGTGACATACCTCTGCTAGAAACTCCTGTC
GGCAGCGAGAGCTGCACTCGGACAGAGCTAGACACTCATTGAGCTTGGCCAAAGGTTGACCA
CTACTCTCTTACTCTAACAGCACATGAATAGAAAGATACTTCTCTCAAGATGGACCCGGTAAATAACCACAA
GGAAGGAAACTGGGTGCGTTACTGAGTTGGGTTCTAATCTGTTCTGGCTGATCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCAGTAAACGCCGTGCTGGGCGCTGTGAAGCCAGCATGTTACCACTGGTC
CAGCAGCCACGACAGCACATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGCGGGAAACCA
GAAAAGGCTTCTACACAGCAGCCTTACTTCATGGCCCACAGACACCACCGCAGTTCTCTAAAGGCTCTG
TGATCGGTGTTGCACTGAGCTTTGGATCAGCATTGTTGATTTGATTTGAAACACAAACAAATCAGGAAG
GTAAATTGGTTGCTGAAAGAGGGATCTGCTGAGGAACCCCTGCTTGTCCAACAGGGTGTCAAGGATTTAAGGAAA
ACCTTCGCTTCTAGGCTAACTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTGTTATTAAAGGTT
TACATCTAAATTGGTCAAGGATGTATTGATTATTGAAAGAAAATTCTATTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTGGGAAAGGTTCAACTTAAGGTTAGAAGTCTAACAGCTACTAGTGTAAAT
TGGAAATATCAATAATTAGAGTATTGACCCAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTCT
CACACAAGTTTACGCTTTTCAAGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATCCAGTTAAGCAATGTTGAAATCAGTTGCTATCTCTCAAAGAAACCTCTCAGGTTAGCTTGAAC
GCCCTCTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAACGCCCTCAGATGTACACAGATG
CCAGTCAGCTCTGGGTTGCCAGGCCCGCTCTAGCTCACTGTTGCCGCTGCTGCCAGGAGGCCCT
GCCATCTTGGGCCCTGGCAGTGGCTGTGCTCCAGTGGCTTACTCACGTTGCCCTGCTTCACTCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTTAGCTGCTCCAGCTTGGGCTCTGTAACAGACCT
TTTGGTTATGGATGGCTACAAAATAGGGCCCCCAATGCTATTGTTTTTTAAGTTGTTAATTATTGTT
AAGATTGCTAAGGCAAAGGCAATTGCAATCACTGTCAGTACAAGTACAATTAACATTGTTAAAGAAAATGGAT
CCCACCTGTTCTTGGCCACAGAAGAACGACCCAGACGCCACAGGCTCTGCGCATTCACAAACAAACATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAAGGTGGAGCAGCCAGGTGAAAGGCCCTGGGGGGAGGAAAG
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGCCGGAGACACTGCTCCATT
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGCTGCC
GAATGGCTCTCACTACTCACCTGTCTTCACTGCTTCCAGTGTCTGGGTTTTTATACCTTGACAGCTTTTTT
AATTGCAATCATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCAGGCCAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTCTGCTGCACTGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCACTGCTCCAGCCT
CTTGGTTGTCTAGTGTAGAGGGTAGCCTTATTGCCCTCTTATACCTAAACCTTCTACACTAGTGC
TGGGAACCCAGGTGAAAGAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTGAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTTATAAAAGCTCAAAAAACCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLIKWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267